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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: gb_ba:*
2: gb_htg:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	ហ	4	ω	2	L	Result No.
712.4	727	727	876.2	876.2	961.8	1279.8	1491	1919.4	1919.4	2244.6	2262.4	2262.4	2262.4	2497.2	2566.4	2566.4	2566.4	2679	Score
26.6	27.1	27.1	32.7	32.7	35.9	47.8	55.7	71.6	71.6	83.8	84.4	84.4	84.4	93.2	95.8	95.8	95.8	100.0	Query
4846	816	816	2186	2186	2257	6235	3194	2448	2448	3181	3138	3138	3138	3189	2639	2639	2639	2679	Query Match Length
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BC064721	BD148820	AX868758	AK054917	AX713476	AK090948	BD183291	BC049792	AK097671	AX834949	AX405642	AK001658	BD156548	AX877222	BC012072	AK027687	BD156534	AX877194	AF170724	ID
BC064721 Xenopus t	BD148820 Primer fo	AX868758 Sequence	AK054917 Homo sapi	AX713476 Sequence	AK090948 Homo sapi	BD183291 Novel gen	BC049792 Mus muscu	АК097671 Ното варі	AX834949 Sequence	AX405642 Sequence	AK001658 Homo sapi	BD156548 Primer fo	AX877222 Sequence	ВС012072 Ното варі	AK027687 Homo sapi	BD156534 Primer fo	AX877194 Sequence	AF170724 Homo sapi	Description

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54.8	55.4	55.6	60	64.4	69.4	82.2	82.8	85.2	93.4	100.4	108.2	139.2	142.4	218	416	430.4	440.8	440.8	488.8	488.8	583	583	608.4	608.4	711.4
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AF429315 Homo sapi	AE001394 Plasmodiu	AF429315 Homo sapi	CQ536585 Sequence	AC021646 Homo sapi	BV002855 S208P6639	AX385952 Sequence	AC087142 Mus muscu	AC087159 Mus muscu	AC092490 Homo sapi	BV168191 sqnm7638	BV180578 sqnm11034	AC118260 Mus muscu	AC125898 Rattus no	AC023047 Homo sapi	AC126301 Rattus no	AC128407 Rattus no	AC106441 Rattus no	AC139591 Rattus no	BD153851 Primer fo	AX873789 Sequence	BD148838 Primer fo	AX868776 Sequence	AC023047 Homo sapi	AC127070 Homo sapi	CQ719982 Sequence

ALIGNMENTS

	CDS	FEATURES source	TITLE DO JOURNAL SI PI	PUBMED 10 REFERENCE 2 AUTHORS H	-	RS CE	MSI S	RESULT 1 AF170724 LOCUS DEFINITION HACCESSION AND AND AND AND AND AND AND AND AND AN
/HOUSESCRICTION FIRA COMMAIN AND LINES LINES LINES (/COGON_START=1 /COGON_START=1 /COGON_START=1 /protein_id="ASF11084.1" /protein_id="ASF11084.1" /db_xref="G1:9651170" /db_xr	"sapiens": 9606"	Location/Qualifiers 12679	Direct Submission Submitted (21-JUL-1999) Wistar Institute, 3601 Spruce Street, Philadelphia, PA 19104, USA	20388685 10935642 2 (bases 1 to 2679) Halazonetis,T.D. and Scolnick,D.M.	THE CHARLES A HILOUIC BLIEBS CHECKPOINT THAT GETAYS CHELY THEO METAPHASE Nature 406 (6794), 430-435 (2000)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2679) Scolnick, D.M. and Halazonetis, T.D. Chfr defines a mirotic stress checknoint that delays entry into	22	AF170724 HOMO Sapiens cell cycle checkpoint protein CHFR mRNA, complete cds. AF170724 AF170724.1 GI:9651169

KVRRSFSDEEGSSEDLLELSDVDSESSDISQPYVVCRQCPEYRRQAAQPPHCPAPEGE

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901 CAGTTGTTGGTCGCACAACCGCGTAGAAATGCCCAAACCGTCCACGAGGACGTCAGAGCA 960	841 GAGGATTTGGAGCCCGTGAAGAAAATGAGAGAGAATGGGGACCTTGACCTGAACGGG 900 	781 GCCTCAGCTCTCCCAGACAGAAAAGACTGCGTCCTTTTCGTCGTTGGAACCCCCAGGATCAG 840	721 GGTGGCATCTCCCCTAAAGGAAGTGGTCCCTCTGTGGCAAGTGATGAAGTCTCCCAGCTTT 780	661 TCTTCCACGGAGCCTTCTCCTGCAGGGCGAGAGCGTTCCTCCAGTTGTGGGGTCTGGGGGT 720	601 TGCTTTGAGGAACCACAGCCATCAACATCGACGTCAGACCTCTTCCCCACAGCCCTCGGCC 660	541 GCAGGTGCAGGGCGAGGGGCCGATCCCCGGGTCCCCTCCGTCGTCGCCCGCC	481 CAAGAATCCTTTGAAGCTAACAAGGAAAATGTGTTCCATGGGACCAAAGATACCTCAGGT 540	421 GAACCGGAACACACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGACA 480	361 AAGAAGCAGACATGCCCTTTACAGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAAT 420	301 CAGGTGACACTGGAAGATACCAGCACCAGTGGAACAGTGATTAACAAGCTGAAGGTTGTT 360 	241 CCCAGCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGGT 300 	181 GTCCTCCTGAGGAAGCGGGAGTGGACCATCGGGCGGAGACGAGGTTGCGACCTTTCCTTC 240	121 CCGCCGCCGCAGCCCTGGGGACGGCTCCTGCGTCTGGGCGCGAGGAGGAGGAGGCCGCAC 180	61 GTTCGGCGCGGGGGGGATGTGAATCCCGATGGAGGGCCCGAGGAAGGCAAGCAGTCG 120	1 AAGAATTCGGCACGAGGCCGCAATGTCTCTTGACAGCGGCGGCGGCGGCGGGTTCCGG 60 	Query Match 100.0%; Score 2679; DB 9; Length 2679; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 2679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PGAPQALGDAPSTSVSLTTAVQDYVCPLQGSHALCTCCFQPMPDRRAEREQDPRVAPQ QCAVCLQPFCHLYMGCTRTGCYGCLAPFCELNLGDKCLDGVLNNNSYESDILKNYLAT RGLTMKNMLTESLVALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASE LPVAVTSRPDCYMGRNCRTQVKAHHAMKFNHICEQTRFKN"
Db	Q B 4	S B 8	? ₽ Q	B &	Ωy Db	Db	₽ Ş	P 5	B 8) p Q	} B &	S B S) b 6	og 43	5 p 6	}	D Qy
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Sequence 12099 :
AX877194
AX877194.1 GI:
                                                                                                             Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto, Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 12099 07-FEB-2001;
Research Association for Biotechnology (JP)
Location/Qualifiers
                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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/db_xref="taxon:9606"
                                               note="unnamed protein product"
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GCDLSFPSNKLVSGDHCRIVVDEKSGQVTLEDISTSGTVINKLKVVKKQTCPLQTGDV
IYLVYRKNEPEHNVAYLYESLSEKQMTQDSFDTSCAAGAGRADPRVPESSPATQVCF
EEPQPSTGTSDLFPTASASSTESSPAGRERSSCCSGGGGISPKGGGSVASDEVSSF
ASALPDRKTASFSSLEPQDOEDLEPVKKKMRGDGDLDLNGQLLVAQPRRNAQTVHEDV
RAAAGKEDKMESTLTCIICQDLLHDCVSLQPCMHTPCAACYSGMMERSSLCFTCRCFV
ERICKNHILINILVEAYLIQHPDKGRSEBIVQSMDARKITQDMLQPKVRRSFSDEEGS
SEDLLELSDVDSESSDISQPYVVCRQCPBYRRQAAQPPHCPAPEGBEGAPQALGDAPS
TSVSLTTANQDYVCPLQGSHALCTCCFQPMPDRRAEREQDERVAPQCCAVCLQPFCHL
YMGCTRTGCYGCLAPFCELNLGDKCLDGVLNNNSYESDILKNYLATRGLTMKNMLTES
LVALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASELPVAVTSRPDCY
WGRNCRTQVKAHHAMKFNHICEQTRFKN"

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                    ACAGAAAGACTGCGTCCTTTTCGTCGTTGGAACCCCAGGATCAGGAGGATTTTGGAGCCCG
                                                                                    AAGGAAGTGGTCCCTCTGTGGCAAGTGATGAAGTCTCCAGCTTTGCCCTAGCTCTCCCAG
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ACAGAAAGACTGCGTCCTTTTCGTCGTTGGAACCCCAGGATCAGGAGGATTTTGGAGCCCG
                                                                   AAGGAAGTGGTCCCTCTGTGGCAAGTGATGAAGTCTCCAGCTTTGCCTCAGCTCTCCCAG
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nilarity 98.6%;
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	CO		RE		VE	RE BD LO	Db	Q D	Q B 4	S B 8	}	Q & &	D Q	P &	D	2 B 8	. p 9	P 5	ם ב
		TITLE	REFERENCE AUTHORS	ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 3 BD156534 LOCUS DEFINITION	26			n in i	ı iv i	א א פ	א גא י) N N	, N. N	<i>a</i>	א נא נ	o + +	
PF 28-UUL-2000 JP 2000280990	HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191363-A/11377	Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primer for synthesizing full-length CDNA and use thereof Patent: JP 2002191463-A 11377 09-JTN-2002.	<pre>maimidia: butheria; rimaces; catarrhin; hominidae; homo. 1 (bases 1 to 2639) Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,</pre>		BD156534 BD156534.1 GI:27862292 JP 2002191363-A/11377.	BD156534 2639 bp DNA linear PAT 17-JAN-2003 Primer for synthesizing full-length CDNA and use thereof.	609 TTGACTAAAA 2618	TCTAATAAGATTTAAATGTCACAAACTGTAGCACAAATAATATAATTTATAATTTACAAA	TCTAATAAGATTTTAATGTCACAAACTGTGTAGCACAATAATATATTTTATTTTATTATTATTATTATTATTA	**/ ACALICII: CACSAGNASSOSCAINAGII: ACASCCIANGGANG IACACARIAICCIG 2336	GTTAMACCAGANGTCTGTTTTCAGGAAAAGTTTCAAGGGAGAAGGGCAAGTTTATCAAAA	CATGCGGCCGTCCGCCGAAGGGCAGTTTTGCTCTTTTTGTACATTTTCCGAAACTACA	TesTBARGCCTEGECAGGECTCGTGGTGGCATCAGCAGCAGCAGCAGCCTTTCTGTAA	AGCTITITACCCTCTGAGTGAGACCCTCCCCAGAGCCCCGGGGCGCAGCCGCCCTCC	GCCCCCTGAGGAAAGGAACGCAGGGGTCTCCGACAGGTGCTCTGGGGTGACTCTTCTGTGG	SOGNOS I SAASKAASUS ISI I I I IAAAA I ALASKAALARSCAC SI CAAGSISTI I I CACA	TCTGTGAACAGGTTCAAAAACTAAGCATCCAGAGGCCCTGAGCAGCTTTCAGCAC	ACTGGGGCCGTAACTGCCGCACTCAGGTGAAAGGTCACCACGCCATGAAATTCAATCATA	

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PI SAITO,

PI SAITO,

PI JUNICHI YAMAMOTO, SHIZUKO ISHLI, ...

PI KEIICHI NAGAI, TETSUJI OTSUKI

PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/00, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00

PC C12P21/02, C12Q1/68//C12P21/08, C12N15/00, C12N15/00
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JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
KEIICHI NAGAI,TETSUJI OTSUKI
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                          AK027687.1 GI:14042552
Oligo capping; fis (full insert
Homo sapiens (human)
Homo sapiens
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Homo sapiens cDNA FLJ14781 fis, to TRANS-ACTING TRANSCRIPTIONAL
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                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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clone NT2RP4000455,
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Negabari, Vamamoto J. Saito K. Kawai, Y. Ioono Y. Nakamura Y. Nakamura Y. Shiratori, A. Sudo, H. Hooditi, T. Naku, Y. Schaira, Hegs Kondo, H. Shiratori, A. Sudo, H. Hooditi, T. Naku, Y. Schaira, Hegs Kondo, H. Shiratori, A. Sudo, H. Hooditi, T. Naku, Y. Schaira, Hegs Kondo, H. Shiratori, A. Sudo, H. Hooditi, T. Naku, Y. Schaira, H. Kondo, H. Sigawara, M. Takhashi, T. Nawai, Y. Schaira, H. Kiakaa, E. Omura, Y. Abe, K. Kathara, K. Katsata, M. Star, K. Tarikawa, K. Etjimozi, K. Tanii, H. Kiaata, M. Watanabe, M. Matanabe, M. Natika, H. Janase, T. Momira, Y. Golya, S. Komai, F. Hara, R. Hara, H. Hara, H. Janase, T. Momira, Y. Golya, S. Komai, F. Hara, R. Hara, H. Janase, T. Momira, Y. Golya, S. Komai, F. Hara, R. Hara, H. Janase, T. Momira, Y. Golya, S. Komai, F. Hara, R. Hara, R. Janase, T. Momira, Y. Golya, S. Komai, F. Hara, R. Hara, R. Hara, H. Janase, T. Momira, Y. Golya, S. Komai, F. Hara, R. Hara, R. Janase, T. Momira, Y. Golya, S. Komai, F. Hara, R. Hara, R. Janase, T. Momira, Y. Golya, S. Komai, F. Hara, R. Janase, T. Momira, Y. Golya, S. Komai, F. Hara, R. Janase, T. Momira, Y. Goloo, Y. Shimita, T. Kathashi, Y. Makashi, M. Matanabe, K. Janase, M. Masana, S. Sandi, H. Janase, M. Masana, S. Sandi, H. Janase, M. Matanabe, K. Janase, M. Masana, C. Janase, M. Matanabe, T. Janashi, M. Janase, M. Matanabe, T. Janashi, M. Janase, M. Matanabe, T. Janashi, M. Janase, M. Matanabe, M. Matanabe, M. Janase, M. Matanabe, M. Janase, M. Matanabe, M. Matanabe, M. Janase, M. Matanabe, M. Matanabe,
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Strausberg, R. D., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R. D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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Homo sapiens checkpoint with forkhead and ring finger domains, mRNA
(cDNA_clone MGC:19963 IMAGE:4650348), complete cds.
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3189)
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BC012072.1 GI:15082329
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and monre of DNA seconds
                       Steven Jones, Jennifer Agano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.Contact: MGC help desk
George Yang, Scott Zuyderduyn, Marco Marra.
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                                                                                                                                                                                                                                                                                                                                                    info@bcgsc.bc.ca
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COMMENT

PUBMED REFERENCE AUTHORS

MEDLINE JOURNAL TITLE

TITLE JOURNAL

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLLL at: http://image.llnl.gov Series: IRAL Plate: 29 Row: n Collumn: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8922674. Location/Qualifiers

FEATURES

source /codon_start=1
/product="CHFR protein"
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/protein_id="AAH22072.1"
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/db_xref="LocusID:55743"
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gene

CDS

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SEDLLELSDDVSESSDISQPYVVCRQCPEYRRQAQPPHCPAPEGEPGAPQALGDAPS
TSVSLTTAVQDYVCFLQGSHALCTCCFQPMEDRRVEEQDFRVAPQCCAVCLQPFCHL
YMGCTRTGCYGCLAPFCELNLGDKCLDGVLNNNSYESDILKNYLATRGLTWKNMLTES

863		Qy 743 GTG pb 625 GTG	Qy 683 CAG Db 565 CAG	Qy 623 CAA Db 505 CAA	Qy 563 ATC	Qy . 503 AGG Db 411	Qy 443 ACC Db 361 ACC	Qy 383 AGA Db 301 AGA	Qy 323 GCA Db 241 GCA	Qy 263 GAG Db 181 GAG	Qy 203 GGA Db 121 GGA	Qy 143 GGC 	Qy 83 GAA Db 1 GAA	Query Match Best Local Similarity 98.5%; Matches 2545; Conservative	ORIGIN	misc_feature		misc_feature
	7 80	GTGGTCCCTCTGTGGCAAGTGATGAAGTCTCCAGCTTTGCCTCAGCTCTCCCAGACAGA	CAGGGCGAGAGCGTTCCTCCAGTTGTGGGTCTGGGGTGGTGGCATCTCCCCTAAAGGAA 742 	CAACATCGACGTCAGACCTCTTCCCCACAGCCTCGGCCTCTTCCACGGAGCCTTCTCCTG 682	ATCCCCGGGTCCCTCCGTCGTCGCCCGCCACTCAGGTGTGCTTTGAGGAACCACGCCACT 622	AGGAAAATGTGTTCCATGGGACCAAAGATACCTCAGGTGCAGGTGCAGGGCGAGGGCCG 562	ACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGACACAAGAATCCTTTGAAGCTAACA 502	AGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAACCGGAACACAACGTGGCAT 442 	GCACCAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCTTTAC 382	GAGATCACTGTAGAATTGTAGTGGATGAAAATCAGGTCAGGTGACACTGGAAGATACCA 322 	GGACCATCGGGCGGAGACGAGGTTGCGACCTTTCCTTCCCCCAGCAATAAACTGGTCTCTG 262	GGCTCCTGCGTCTGGGCGCGGAGGAGGGCGAGGCCGCACGTCCTCCTGAGGAAGCGGGAGT 202	GAATCCCGATGGAGCGGCCCGAGGAAGGCAAGCAGTCGCCGCCGCCGCAGCCCTGGGGAC 142	93.2%; Score 2497.2; DB 9; Length 3189; larity 98.5%; Pred. No. 0; Conservative 0; Mismatches 3; Indels 36; Gaps 1;	·	/db_xref="CDD:pfam00498" 8791010 /gene="CHPR" /note="HRD1; Region: COG5243, HRD1, HRD ubiquitin liqase	<pre>/gene="CHFR" /note="FHA; Region: FHA domain. The FHA (Forkhead-associated) domain is a phosphopeptide binding motif"</pre>	LVALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASELPVAVTSRPDCY WGRNCRTQVKAHHAMKFNHICEQTRFKN" 120. 317
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1943 AGAACATTCCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGG 2002	1883 CCGTTCTGTGTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGC 1942	1705 GCCTCGTGGCTCTCCAGCGGGAGTGTTTCTGCTGTTTGATTACAGAGTCACGGGAGACA 1764	CCATCCT WANGART LACC I GGCARC CAGNOGI I GARCA I GGARCARANCA I GI I GARCAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ACCITCANCCISES ISACAMSIS ICITES ACGREGAS CONCENTANCA CANCARCAS CAN	GCCACCIGIACIGNOSCICCACCIGNACIGNOSCICCIGNACIGNOSCICCIGNICIGNACIGNACIGNACIGNACIGNACIGNACI	ASCREGARCE ASSECT CONTROL OF THE CON		SCHIECTICATES TO STATE TO STAT	CGCCGCAGCCTCCCACCTCCCAGCACCACACACACACACTTTACCCCACAGGCCCTCCCCACAGGCCCACAGGCCCACAGGACCCCACAGGCCCTTGGCCCACAGGCCCACAGGCCCACAGGACCCTTGGCCCACAGGCCCACAGGCCCACAGGACCCTTGGCCCACAGGCCCACAGGCCCACAGGACCCTTGGCCCACAGGACCCCACAGGACCCCACAGGACCCCTTGGCCCACAGGACCCCTTGGCCCACAGGACCCCACAGGACCCCACAGGACCCCTTGGCCCACAGGACCCCACAGGACCCCACAGGACCCCTTGCACAGACGACCTTTACACACAGACTTTACACACAGACTTTACACACAGACTTTACACACAC	1343 CELCAGACATIAGECARCGECARGGECGAGGGCCAGGGCCCAGGACCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCAGGGCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCAGGGCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGGCAGGGGCAGGGGGG	111CLOSA GARGARAGGONG I CARANGARCE IGE I GGAGE IG I CARANGEJ I GARCAGI GANGE I I LITA I I I I I I I I I I I I I I I I I I	GTATGGATGCCAGGATTAAATCACTCAAGACATCCTGCAGCCAAAGTCAGGCGGTCTT	TOTTGRANGCATACCICATCCAGCATCCAGACAAGAGTCGCAGTGAAGAAGATGTGCAAA	TGTGTCCTACCTGCCGCTGTCCCGTGGAGCGGATCTGTAAAAACCACATCCTCAACAACACACAC	1043 AGCCCTGCATGCACACGTTCTGCGCGGCTTGCTACTCGGGCTGGATGGA	983 TGGAGGAGACGCTGACATGCATCATCTGCCAGGACCTGCTGCACGACTGCGTGAGTTTGC 1042	923 GTAGAAATGCCCAAACCGTCCACGAGGACGTCAGAGCAGCGGCTGGGAAGCCAGACAAGA 982 	

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SOURCE
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KEYWORDS
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ACCESSION
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Sequence 12127 from Pat
AX877222
AX877222.1 GI:40031958
                                                         Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., S
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K.
Primers for synthesising full-length cDNA and
Patent: EP 1074617-A 12127 07-F3B-2001,
Research Association for Biotechnology (JP)
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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	1827 CGTGGCTCTCCAGCGGGAGTGTTTTCTGCTGTCTGATTACAGAGTCACGGGAGACACCGT 1886	Ś
TITLE Primer for a	1618 CCTGAAGAATTACCTGGCAACCAGAGGTTTGACATGGAAAAACATGTTGACCGAGAGCCT 1677	В
REFERENCE 1 (bases 1 AUTHORS Ota, T., Isoc	1767 ССТВАЛБАЛТТАССТВЕСЛАССЛЕВЕСТТВАСАТВЕЛАЛАЛАСЛІВТВАССВАВЛЕСТ 1826	á
	1707 CAACCTGGGTGACAAGTGTCTGGACGGCGTGCTGAACAACAACACCTACGAGTCAGACAT 1766 	<u> </u>
KEYWORDS JP 200219136 SOURCE Homo sapiens		Ъ
ACCESSION BD156548	1647 CCTGTACTGGGGCTGCACCCGGACCGGCTGCTACGGCTGCCTGGCCCCGTTTTGTGAGCT 1706	Ş
BD15654	1587 CGAGCAGGACCCGCGTGTCGCCCCTCAGCAGTGTGCGGTTCTGCCTGC	ß &
Db 2456 TTTAAATGTC	1378 AGGAAGCCACGCCTGTGCACCTGCTTGCCAGCCCATGCCCGACCGGAGAGCGGAGCG 1437	뭣
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Db 2396 AACCACAGC	TGCACCCCCACGTCAGCCTGACAGCAGTACTAGGATTACGTGTGCCCTCTGCA	문 5
Qy 2547 AACCACAGC	へいちにしょうしつ としにしょうしゃ にしょうしゅう マン・ドラン・スター・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・	5
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2487	1198 AGACATTAGCCAGCCATACGTCGTGTGCCCGCAGTGTCCTGAGTACAGAAGGCAGGC	망
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2367	.287 TGATGAAGAAGGGAGTTCAGAGGACCTGCTGGAGCTGTCAGACGTTGACAGTGAGTCCTC	Ś
Db 2156 TGGGCAGGG	127 GGATGCCAGGAATAAAATCACTCAAGACATGCTGCAGCCCAAAGTCAGGCGGTCTTTTTC 1286 127 HIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	<u> </u>
Фу 2307 Теееслеее	GGAAGCATACCTCATCCAGCATCCAGACAAGAGTCGCAGTGAAGAAGATGTGCAAAGTAT	, B
	GGAAGCATACCTCATCCAGCATCCAGACAAGAGTCGCAGTGAAGAAGATGTGCAAAGTAT	ঠ
Db 2038 GGAAGGGACC		皮
Qy 2187 GGAAGGGACC	TCCTACCTGCCGCTGTCCCGTGGAGCGGATCTGTAAAAACCACATCCTCAACAACCTCGT	Ś
1978	1047 CTGCATGCACACGTTCTCGGCGGCTTGCTACTCGGGCTGGATGGA	8 8
2127	838 GGAGACGCTGACATGCATCTGCCAGGACCTGCTGCACGACTGCGTGAGTTTGCAGCC 897	문
	987 GGAGACGCTGACATCCATCATCTGCCAGGACCTGCTGCACGACTGCGTGAGTTTGCAGCC 1046	Ś
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Qy 2007 TAACTGCCG	AAATGCCCAAACCGTCCACGAGGACGTCAGAGCAGCGGCTGGGAAGCCAGACAAGATGGA	§
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DISG548.1 GI:27862306
DISG548 synthesizing 3138 bp DNA linear PAT 17-JAN-2003 full-length cDNA and use thereof. Euteleostomi;

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FEATURES
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PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU SAITO,
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/09 CC
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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                                                                                                                                                                                                                     CTGTGTTGCCCAGGCTGGTCTAAAACTCCTGGGATCAAGT---------
                                                                                                                                                                                                                                                AAATGTGTTCCATGGGACCAAAGATACCTCAGGTGCAGGTGCAGGGCGAGGGGCGATCC
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                                                                                                                                ATCGACGTCAGACCTCTTCCCCACAGCCTCGGCCTCTTCCACGGAGCCTTCTCCTGCAGG
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mer for synthesizing full-length cDNA and use thereof FH F Location/Qualifiers

CDS (65). (1933).

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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   CGTGGCTCTCCAGCGGGAGTGTTTCTGCTGTCTGATTACAGAGTCACGGGAGACACCGT
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                                                                                                                                                            AK001658.1 GI:7023050
oligo capping; fis (full insert sequence)
Homo sapiens (human)
Homo sapiens
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Homo sapiens cDNA FLJ10796 fis, to TRANS-ACTING TRANSCRIPTIONAL
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Mammalia, Eutheria; Primates;
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Catarrhini; Hominidae;
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one NT2RP4000648,
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COMMENT

FEATURES

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Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, B., Omura, Y., Abe, K., Kamihara, K., Kateuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Pujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Saishihata, N., Sano, S., Moriya, S., Moniyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakiami, B., Yanazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hizao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nakajima, Y., Kikuchi, H., Masuho, Y., Yamashita, R., Nakaii, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human COMAs
                                                                              Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomice Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (R-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' - & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
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Isogai,T. and Otsuki,T.
Direct Submission
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AUTHORS

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2007 TAACTIGCCGCACTCAGGTGAAAGCTCACCCACGCCATGAAATTCAATCATAATCTGTGAACA 2066	1997 TURISTIACISCISTICGCAGCTICGGGAGGTGACCTATCAGTATGGCAGAA 1946	827 CGTGGCTCTCCAGCGGGAGTGTTTCTGCTGTCTGATTACAGAGTCACGGAGAGACACCGT	1558 CAACCTGGGTGACAAGTGTCTGGACGGCGTGCTGAACAACAGCTACGAGTCAGACAT 1617 1767 CCTGAAGAATTACCTGGCAACCAGAGGTTTGACATGGAAAAACATGTTGACCGAGAGGCCT 1826		GAGCAGGACCCGCGTGTCGCCCCTCAGCAGTTGTCCGGTCTGCCGTGCAGCCTTTTCTGCCA	AGGAAGCCACGCCCTGTGCACCTGCTGCTCCAGCCCATGCCCGACCGGAGAGCGGAGCG			1347 AGACATTAGCCAGCCATACGTCGTGTGCCGGCAGTGTCCTGAGTACAGAAGGCAGGC	1287 TGATGAAGAAGGGAGTTCAGAGGACCTGCTGGAGCTGTCAGACGTTGACAGTGAGTCCTC 1346					

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0b	δ	ф	\$	Db	Q	рь	Ş	рь	Ş	מע	ļ (? !	} &	ΔР	Ş	Db	Ş	DЪ	γŞ	ΩЬ	β	DЬ	Ą	Db ,	ş	당 :	Q	Дb	δ	Db	\$	Best Local Matches 24	Query Ma	ORIGIN		
798 CAACCGCGTAGE	916 CAACCGCGTAG	 738 GTGAAGAAGAA	856 GTGAAGAAGAA	678 GACAGAAAGAC	796 GAÇAGAAAGAC	618 AAAGGAAGTGG	736 AAAGGAAGTGG	591	676 TCTCCTGCAGG		en caecunicand		556 GGGGCCGATCC	501 ATGGTGCCTTG	496 GCTAACAAGGA	441 GTGGCATACCT	436 GTGGCATACCT	381 CCTTTACAGAC	376 CCTTTACAGAC	321 GATACCAGCAC	316 GATACCAGCAC	261 GTCTCTGGAGA	256 GTCTCTGGAGA		196 CGGGAGTGGAC		136 TGGGGACGGCT	81 GGGATGTGAAT	76 GGGATGTGAAT		16 GGCCGCAATGT	cal Similarity 2447; Conserva			LNNNS	YRRQ

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85	CAACCGCGTAGAAATGCCCAAACCGTCCACGAGGACGTCAGAGCAGCGGCTGGGAAGCCA	798	B 1
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–ი	GACAGAAAGACTGCGTCCTTTTCGTCGTTGGAACCCC	796	Ş
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	AAAGGAAGTGGTCCCTCTGTGGCAAGTGATGAAGTCT	736	Ş
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	CTGCAGGGCGAGAGCG	676	ξ.
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GACCAAAGATACCTCAGGTGCAGGTGCAGGGCGA 555	GCTAACAAGGAAAATGTGTTTCCATGGGACCAAAGATA	496	Ş
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CTTGGTGTACAGGAAGAATGAACCGGAACACAAC 435	CCTTTACAGACTGGGGATGTCATCTACTTGGTGTACA	376	Ş.
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GAGCCGCACGT	TGGGGACGGCTCCTGCGTCTGGGCGCGGAGGAGGGCC	141	맑
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gcggcgcagccggrrccgggrrcagcgcgaggcg 75	ggccgcaangrcrcrraacagcggcggcggcagcc	σ	Ş
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ACHINGUS SOURCE SOURCE ORGANISM Homo sapiens Enkarycta; Me Mammalia; Eut REFERENCE 1 Isogai,T., St Yamamoto,J.I. TITLE JOURNAL Fatent: EP 13 FEATURES FEATURES FEATURES FOURMAL Research Assort Source FOURMAL Research Assort Local Source JOURNAL Research Assort JOURNAL Research Assort Local Source JOURNAL Research Assort Local Source JOURNAL Research Assort Local Mb ORIGIN ORIGIN	OR PE SA	GAGTCAGACATCCTGAAGAATTACCTGGCAACCAGAGGTTTGACATGAAAAACATGTTG
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y 2356 ACATTCCGCCO b 2236 ACATTCCGCCO y 2416 AGTTAAAGCA y 2416 AGTTAAAGCG b 2296 AGTTAAAGCG y 2476 AACATTGTTTT y 2476 AACATTGTTTT b 2356 AACATTGTTTTT	40 40 40 40 40	1276 CGGTCTTTTTCTGATGAAGGAAGGAGGTTCAGAGGACCTGCTGAGACCTTGAC 1335
y 21/6 AGCCCCCTGA	20 DD C4	1096 TCGTCCCTGTGTCCTACCTGCCGCTGTCCCGTGGAGCGGATCTGTAAAAACCACATCCTC 1155
2056 1938 1998 1998	Q D D Q Q	976 GACAAGATGGAGGAGACGCTGACATGCATCTGCCAGGACCTGCTGCACGACTGCGTG 1035

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                                                                                          Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuho,Y.
Full-tength cDNA sequences
Patent: EP 1347046-A 2073 24-SEP-2003;
Research Association for Biotechnology (JP)
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Sequence 2073 from Patent EP1347046.
AX834949 AX834949.1 GI:39921084
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2448 bp mRNA linear PRI 30-JAN-2004
Homo sapiens cDNA FLJ40352 fis, clone TESTI2033505, highly similar
to Homo sapiens cell cycle checkpoint protein CHFR mRNA.
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Isogai, T. and Yamamoto, J.
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Submitted (04-7UL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:s1-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Rey Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB. Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamateu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Sato,H., Washikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Magatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.

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Indels 284; Length 2448

GACGAGGTTGCGGACCTTTCCCTTCCCCAGCAATAAACTGGTCTCTGGAGATCACTGTAGAA 277 CCTCCAGTTGTGGGTCTGGGGGTGGTGGCATCTCCCCTAAAGGAAGTGGTCCCTCTGTGG 757 CGTCGTCGCCCGCCACTCAGGTGTGCTTTGAGGAACCACAGCCATCAACATCGACGTCAG ATGGGACCAAAGATACCTCAGGTGCAGGTGCAGGGCGAGGGGCCGATCCCCGGGTCCCTC 577 TAAGTGAAAAGCAAGGCATGACACAAGAATCCTTTGAAGCTAACAAGGAAAATGTGTTCC TCTACTTGGTGTACAGGAAGAATGAACCGGGAACACAACGTGGCATACCTCTATGAATCTT TGATTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCTTTACAGACTGGGGATGTCA TGATTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCTTTACAGACTGGGGATGTCA 397 TTGTAGTGGATGAAAAATCAGGTCAGGTGACACTGGAAGATACCAGCACCAGTGGAACAG 337 GACCCTGTTGCGACCTTTCCCTCAGCAATAAACTGGTCTCTGGAGATCACTGTAGAA 142 ACCTCTTCCCCACAGCCTCGGCCTCTTCCACGGAGCCTTCTCCTGCAGGGCGAGAGCGTT 697 TCTACTTGGTGTACAGGAAGAATGAACCGGGAACACAACGTGGCATACCTCTATGAATCTT 457 TTGTAGTGGATGAAAAATCAGGTCAGGTGACACTGGAAGATACCAGCACCAGTGGAACAG TAAGTGAAAAGCAAGGCATGACACAAGAATCCTT-----517 637 322 356 262

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1658 GCTGCACCCGGACCGGCTACCGCTGCCTGGCCCCGTTTTGT	407 CANGTONANCICCAGGATTTGGCTCAGCTCTCCCAGAAAAAAACGCTGCGTCCTTTT 466 818 COTTCGTTGAAACCCCAGGATTCAGGAGAATTTGGAGCCCGTAGAAAAAAACGCTGCGTCCTTTT 466 818 COTTCGTAGACCCCAGGATTGTAGGAGGATTGTTGGAGCCCGTAAAGAAGAAAAAAACGCCAAA 977 818 TAGGGGACCTTGAACCTGAACGGGCTAGGACGATTGTTGGAGCCCGTAAACGAGGAAAAAACGCCCAAA 937 818 TAGGGGACCTTGAACCTGAACGGGCTAGGACGACCAGCGGTAAAAAATGCCCAAA 937 818 CCGTCCACGAAGAACGCTCCAGAACCAGCGTTGGAACGAAC	CAAGTGATGAAGTCTCCAGCTTTGCCTCAGCTCTCCCAGACAGA
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RS Strauberg, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Mizny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnetch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             info@bcggc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Peatherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schmerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 109 Row: 1 Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27370049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (31-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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55.7%; 75.2%; Score 1491; Pred. No. 0 DB 10; Length 3194;

156 GGGCGCGGAGGAGCCGCACGTCCTCCTGAGGAAGCGGGAGTGGACCATCGGGCG 215 AAAGCATTCTTCTAGCTCTGGACCTGGGAACACAAGCATCTCCCCAAAAGGACGCAGTTC 729 AGAGCGTTCCTCCAGTTGTGGGTTGGGGGTGGTGGCATCTCCCCTAAAGGAAGTGGTCC 749 AGACCTCTTCCCCACAGCCTCGGCCTCTTCCACGGAGCC-----TTCTCCCTGCAGGGCG ACTATTGTCACCCATGGCTCAGACATGCTTAGAGGAACCACAGCCATCAACATCGACATC TCCGTCGTCGCCCACTCAGGTGTGCTTTGAGGAACCACAGCCATCAACATCGACGTC AATTGTAGTGGATGAAAAATCAGGTCAGGTGACACTGGAAGATACCAGCACCAGTGGAAC AGACCTCCTCCCCACGGCCTCTACCTCTTCTACGGAGCCAGAGCTGACCTCTGCAGGGCA TTTAAGTGGCAAACAGAGCTTAACTCAAGACTCCCTTGAAGCCAATAAGGAAAATATGTT TTTAAGTGAAAAGCAAGGCATGACAAGAATCCTTTGAAGCTAACAAGGAAAATGTGTT 515 CATCTACTTGGTGTACAGGAAGAATGAACCGGAACACGACGTGGCATACCTCTATGAATC 455 AGTGATTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCTTTACAGACTGGGGGATGT GAGGAGAGGCTGTGACCTCTTTTCCCCCAGCAATAAACTGGTCTCTGGAGATCACTGTAA GAGACGAGGTTGCGACCTTTCCCTTCCCCAGCAATAAACTGGTCTCTGGAGAATCACTGTAG 275 AGGCGCAGAGGAGGACCCCAGATCCTTCTTTGGAAACGCGAGTGGACCATCGGAAG ecececeaceacaeceariceeerreeerreeececeeeceeecearereaarccceareea CCATGGGACCAAAGATACCTCAGGTGCAGGTGCAGGGGCGAGGGGCCGATCCCCGGGTCCC CATCTATTTGGTGTACAGGAAGAATGAGCCAGAACACAATGTGGCATACCTCTATGAATC AGTGATCAATAAGCTGCAAGTTGTTAAGAAGCAGACTTACCCTTTACAGAGCGGGGATAT ACTTACAGTGGATGAAATATCTGGTGAGGTGACACTGGAAGACACCAGCACCAATGGAAC GCTACACGGGAAGAGCAGCCGCCGCCGCCGCAGGAACCCTGGGGGAGGCTTCTTCGTCT gcegccceaegaaegcaaegcaerceccecceccecaeccrieegaacegcrecriecercr 155 GCGGCGACTGTAAGGCCGGTTCCGGGGGTCCGCGCAGGGCGTGGGATGTGAGTCCTATGGA 75 Conservative 0 Mismatches 615; Indels 48; 669 395 315 689 609 635 549 575 495 375 435 335 255 195

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a X	ORGANISM	1767 CCTGAAGAATTACCTGGCAACCAGAGGTTTGACATGGAAAAACATGTTGACCGAGAGGCCT 1826
G G G G G G G G G G G G G G G G G G G	ACCESSION VERSION KEYWORDS	1707 CAACCTGGGTGACAAGTGTCTGGACGGGGTGCTGAACAACAGCTACGAGTCAGACAT 1766
-	RESULT 13 BD183291 LOCUS	1647 CCTGTACTGGGGCTGCACCCGGACCGGCTGCTACGGCTGCCCGGTTTTGTGAGCT 1706
2639 .	Db .	1587 CGAGCAGGACCCGCGTGCCCCTCAGCAGCTGTGCCGGTCTGCCGCAGCCTTTCTGCCA 1646
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7	Db	1527 AGGARACCARCECCTGTGCACCTGCTTCCAGCCCARCCGGACAGCCGAAGCGGAGAGCG 1586
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KAZUSA DNA RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002345492-A/4
PD 03-DEC-2002
PF 26-FEB-2002 JP 2002049009
PI 05AMU OHARA, TAKAHIRO NAGASE, DAISUKE
PC C12N15/09, COTK14/47//A61K31/711, A61K
PC A61P25/18, A61P35/00, C12N15/00, A61K37
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                                                                                                          GCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGGGCCGTAACTGC
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/mol_type="genomic DNA"
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5560 GTCACAAACTGTAGCACAAATAATATATATTTATAATTTACAAATTGACTAAAA 5612	7 2614 GTCACAAACTGTAGCACAAATAATATAATATTAATTTATAATTTACAAATTGACAAAAA 2666	5500 GCATTTTATCTATTTTTATTTTAATAGGTTTGGTGCTTATCTTCTAATAAGATTTAAAT 5559	/ 2554 GCATTTTATCTATTTTATTTTAATAGGTTTTGGTGCTTATCTTAATAAGATTTAAAT 2613	5440 GGGAGCATAAGTTTACAGCCTACAGGACGTACACAATATCCTGCTGCTGCTGGGAAAACCACA 5499	/ 2494 GGGAGCATAAGTTTACAGCCTACAGGACGTACACAATATCCTGCTGCTGGGAAAACCACA 2553	5380 TTTTCAGGAAAAGTTTCAAGGGAAAGGGCAAGTTTATCAAAAAACATTGTTTCAGGAGAA 5439	/ 2434 TTTTCAGGAAAAGTTTCAAGGGAGAAGGGCAAGTTTTATCAAAAAACATTGTTTCAGGAGAA 2493	5320 GAGAGGGGCAGTTTTGCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTG 5379	2374 GAGAGGGGCAGTTTTGCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTG 2433	5260 GGCTCGTGGTGGCATCAGCAGCAGAGACGAAGCCTTTCTGTAACATGCGGCCGTCCCGCC 5319	/ 2314 GGCTCGTGGTGGCATCAGCAGCAGAGACGAAGCCTTTCTGTAACATGCGGCCCGTCCCGCC 2373	5200 GTGAGACCCTCCCCAGAGCCCCGGGGGCCGCAGCCCCCCCTGGTGAGCGCTGGGCAG 5259	2254 GTGAGACCCTCCCCAGAGCCCCGGGGGCCGCAGCCCCTCCTGGTGAGCGCTGGGCAG 2313	5142 ACGCAGGGTCTCCGACAGGTGCTCTGGGGGTGACTCTTCTGTGGAGCTTTACCCTCTGA 5199	/ 2194 ACGCAGGGTCTCCGACAGGTGCTCTGGGGGTGACTCTTCTGTGGAGCTTTTTTACCCTCTGA 2253	5082 TGTTTTTAAAATACAGAGACAAGCACGTCAAGGTGTTTTCACAGCCCCCTGAGGGAAGGG 5141	7 2134 TGTTTTTAAAATACAGAGACAAGCACGTCAAGGTGTTTTCACAGCCCCCTGAGGGAAGGG 2193	5022 TTCAAAAACTAAGCATCCAGAGGCCCTGAGCAGCTTTCAGCACTGGAGGTGAAGAGAGAG

RESULT 14 AK090948 VERSION KEYWORDS SOURCE REFERENCE DEFINITION ACCESSION Pocus ORGANISM

AUTHORS

Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens

Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

AK090948.1 GI:21749208 oligo capping; fis (full Homo sapiens (human) AK090948 2257 bp mRNA linear PRI Homo sapiens cDNA FLJ33629 fis, clone BRAMY2022454, high to Homo sapiens cell cycle checkpoint protein CHFR mRNA. (full insert sequence). PRI 30-JAN-2004 highly similar

Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kinura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Sugawara, M., Yamazaki, M., Ninomiya, K., Tahibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hitaoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Takeuchi, K., Arita, M., Imose, M., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Sano, S., Moriya, S., Momiyama, H., Satoh, M., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Kumarai, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumarai, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumarai, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumarai, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumarai, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumarai, A., Sanoh, A., Mizoguchi, H., Sanoh, A., Mizoguchi, A., Takemoto, S., Moniyan, S., Senoh, A., Watanabe, K., Kumarai, A., Sanoh, A., Wa Sugiyama,A., Takemoto,M., Kawakami,B., Kumagai,A., Itakura,S., Fukuzumi,Y., Fi Komiyama, M.,

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Best Local Similarity
Matches 963; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:s1-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakameteu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human CDNA sequencing project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 2257)
Isogai, T. and Yamamoto, J.
Direct Submission
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                                                                                                                                                                                                              AGCCTCGTGGCTCTCCAGCGGGGAGTGTTTCTGCTGTTCTGATTACAGAGTCACGGGAGAC 1881
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  CAGAACATTCCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGG
                                                                                                                                       ACCGTTCTGTGTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGG 1941
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                                             CAGAACATTCCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGG 2001
                                                                                          ACCGTTCTGTGTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGG
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/db_xref="taxon:9606"
/clone="BRAMY2022454"
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/clone_lib="BRAMY2"
/note="cloning_vector: pME18SFL3"
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Pred. No. 1.7e-211;
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                                                                                     Full-length cDNAs
Patent: EP 1293569-A 160 19-MAR-2003;
Helix Research Institute (JP) ; Resea
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Sequence 160 from Patent
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                                                                                                                                                                             Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
                                                                    Biotechnology (JP)
                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; 
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                             Location/Qualifiers
organism="Homo sapiens"
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2421

PAT

15-APR-2003

Euteleostomi;

Вb	δ	В	Ş	B &	? 5	\$ 8	皮	Ş	음 성	ф	Ş	Db	γ	da Vy	9 8	8	B	Ş	pb 1	Ş	Вb	§	дb	Ş	Db	Ş	Query Maest Low Matches	ORIGIN	
1509 ATGTCACAAACTGTAGCACAAATAATATATAATTTATAATTTACAAATTGACTAAAA 1563	2612 ATGTCACAAACTGTAGCACAAATAATATAATATTATAATTTACAAATTGACAAAAA 2666	1449 CAGCATTTTATCTATTTTTTTTTAATAGGTTTTGGTGCTTATCTTCTAATAAGATTTAA 1508	552 CAGCATTTTATCTATTTTTATTTTAATAGGTTTGGTGCTTATCTTCTAA	1389 AAGGGAGCATAAGTITACAGCCTACAGGACGTACACAATATCCTGCTGCTGGAAAAACCA 2551	329 TGITTTCAGGAAAAGTTTCAAGGAGAAGGGCAAGTTTATCAAAAACATTGTTTCAGGAG 138	432 TGTTTTCAGGAAAAGTTTCAAGGGAGAAGGGCAAGTTTATCAAAAACATTGTTTCAGGAG 249	1269 CCGAGAGGGGCAGTTTTGCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTC 1328	372	2312 AGGGCTCGTGGTGGCATCAGCAGCAGAGACGAAGCCTTTCTGTAACATGCGGCCGTCCCCG 2371	1149 GAGTGAGACCCTCCCAGAGCCCCGGGGGCCCGAGCCCGCCC	2252 GAGTGAGACCCTCCCCAGAGCCCCGGGGGGCCGCAGCCCTCCTGGTGAGCGCTGGGC 2311	1091 GGACGCAGGGTCTCCGACAGGTGCTCTGGGGGTGACTCTTCTGTGGAGCTTTACCCTCT 1148	PAGGGTCTCCGACAGGTGCTCTGGGGGTGACTCTTCTGTGGAGCTTTTTACC	2132 GTGTTTTTAAATACAGAGACAAGCACGTCAAGGTGTTTTCACAGCCCCCTGAGGGAAG 2191	971 GGTTCAAAAACTAAGCATCCAGAGGCCCTGAGCAGCTTTCAGCACTGGAGGTGAAGAGAG 103	72 GGTTCAAAAACTAAGCATCCAGAGGCCCTGAGCAGCTTTCAGCACTGGAGGTGAAGAGAG 21	911 GCGGCACTCAGGTGAAAGCTCACCACGCCATGAAATTCATATCATATCTGTGAACAGACAA 970	င္ပ	851 CTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGGGCCGTAACT 91	20	791 GTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGCAGAACATTC 850	1892 GTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGCAGAACATTC 1951	-	1832 CTCTCCAGCGGGAGTGTTTCTGCTGTCTGATTACAGAGTCACGGGAGACACCGTTCTGT 1891	GA-	AATTACCTGGCAACCAGAGGTTTGACATGGAAAAAACATGTTGACCGAGAGCCT	Match 32.7%; Score 876.2; DB 6; Length 2186; Local Similarity 99.4%; Pred. No. 1.1e-191; les 890; Conservative 0; Mismatches 3; Indels 2; Gaps 1;	/mol_type="unassigned DNA" /db_xref="taxon:9606"	

Search completed: January 15, 2005, 04:02:36 Job time: 11105 secs

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Result
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Aah14542 Human cDN
Aah14556 Human cDN
Abn59646 Novel hum
Aaf89709 Nucleotid
Adm03388 Human pol
Aai88903 Human pol
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Abx73184 Human cDN
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Aah06828 Human cDN
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Aah06838 Human cDN
Aabx73645 Human nov
Aa824304 Human nov
Aa845374 Human sec
Aah11859 Human cDN
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AAF30352;

AAF30352 standard; cDNA; 2679 BP.

Aah71471

ALIGNMENTS

RESULT 1
AAF30352
ID AAF3
XX AAF30
XX AAF3
XX AAF3
XX Chec
CKW Chec
CKW Chec
CKW White
CKW WHITE Checkpoint with forkhead associated domain and ring finger; Chfr; human; mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening; ubiquitin-protein ligase; ss. Novel nucleic acid sequence of mitotic checkpoint gene encoding a checkpoint with forkhead-associated domain and ring finger protein, diagnosing tumorigenic cells and in screening for anticancer drugs. Claim 2(a); Fig 4A-D; 85pp; English. Halazonetis T, Scolnick D; 14-JUN-2000; 2000WO-US016391 08-FEB-2001. mutation Homo sapiens. Human chfr cDNA encoding checkpoint with FHA and ring finger protein. 14-MAY-2001 P-PSDB; AAB20219. WPI; 2001-182927/18. 29-JUL-1999; 99US-0146194P WO200109150-A2 (WIST-) WISTAR INST ANATOMY & BIOLOGY. (first entry) replace (1828, A)

*tag= b

/note= "alters codon GTG (Val)
human cancer cell line U2OS" Location/Qualifiers 91. .2085 ç ATG (Met) ij for

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The present sequence is that of cDNA encoding the human mitotic checkpoint protein Chfr (see AAB20219) having a forkhead associated commain (FHA) and a ring finger domain. The protein is required for regulation of the transition of cells from prophase to metaphase during mitosis. It has ubiquitin-protein ligase activity. The Chfr checkpoint was evident in primary human cells but was inactivated in 4 of 8 human carcer cell lines. In U2OS cells, a mutation was identified, which caused a Val to Met amino acid substitution in the highly conserved C-terminal Cys-rich region of the Chfr protein. In the absence of the Chfr checkpoint, cells subjected to mitotic stress condensed their chromosomes despite failing to separate their chromosomes. Chfr may monitor C centrosome separation. Inactivation of the chfr gene in human cancer is theorized to underlie the increased sensitivity of cancer cells to comprise encoding at least amino acids 31-103, 303-346, 476-641 (or their antisense sequences) are claimed. The chfr cDNA was isolated from an expressed sequence tag database sequence for cDNAs with FHA motifs. C claimed methods of determining the tumourigenic potential of a cell comprise examining the cell for the presence of chfr nucleic acid (absence or mutation indicating predisposition to tumourigensis upon exposure to mitotic stress). Also claimed is a diagnostic agent, e.g. an antisense fragment of the present sequence, that binds to the chfr cancer is a cancer is a ligand selected from an antibody or its fragment. The Chfr may comprise a ligand selected from an antibody or its fragment. The Chfr can anditional antibumour therapsien for drugs which can cancer is inhibit the activity of Chfr and cancer cells. Chfr polypeptides are useful in screening for drugs which can can inhibit the activity of Chfr and cancer cells.
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2641
                                                                         2581
                                                                                                                                                                     GGCAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAGTTTACAGCCTACAGGA
                                                                                                                                                                                                                       ATTTTCCGAAACTACAGTTAAAAGCAGAAGTCTGTTTTCAGGAAAAGTTTTCAAGGGAGAAG
                                                                                                                                                                                                                                                                          CGAAGCCTTTCTGTAACATGCGGCCGTCCCGCCGAGAGGGGCAGTTTTTGCTCTTTTTGTAC
                                                                                                                                                                                                                                                                                                                              CCGCAGCCCCCCCCCCGGTGAGCGCCTGGGCAGGGCTCGTGGTGGCATCAGCAGCAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCTGACCTATCAGTATCGGCAGAACATTCCTGCTTCCGAGTTGCCAGTGGCCGTAACA
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                                                                                                                                                                                                                                                             CGAAGCCTTTCTGTAACATGCGGCCGTCCCGCCGAGAGGGGCAGTTTTTGCTCTTTTTGTAC
                                                                                                                                                                                                                                                                                                                                                                                 GGTGACTCTTCTGTGGAGCTTTTTTACCCTCTGAGTGAGACCCCTCCCCAGAGCCCCCGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGCAGCTTTCAGCACTGGAGGTGAAGAGAGCGTGTTTTTAAAATACAGAGACAAGCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACAACAACAGCTACGAGTCAGACATCCTGGAAGAATTACCTGGCAACCAGAGGTTTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTGCCTGGCCCCGTTTTTGTGAGCTCAACCTGGGTGACAAGTGTCTGGACGGCGTGCTG
              GGTTTGGTGCTTATCTAATAAGATTTAAATGTCACAAACTGTAGCACAAATAATATA
                                                                                                                                                                                                           ATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAGTTTCAAGGGAGAAG
                                                                                                                                                                                                                                                                                                               CCGCAGCCCGCCCTCCTGGTGAGCGCTGGGCAGGGCTCGTGGTGGCATCAGCAGCAGAGA
                                                                                                                                                                                                                                                                                                                                                                   TCAAGGTGTTTTCACAGCCCCCCTGAGGGAAGGGACGCAGGGTCTCCGACAGGTGCTCTGG
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RESULT

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GGATGTGAATCCCGATGGAGCGGCCCGAGGAAGGCAAGCAGTCGCCGCCGCCGCAGCCCT 136 Query Match Best Local Similarity Matches 2613; Conserv

Conservative

0;

<u>+</u> 4.

Indels Length 2639

36;

Gaps

64

95.8%;

Score 2566.4; Pred. No. 0; Mismatches

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CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprises as equence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC complementary strand of a polynucleotide which comprises a 5'-end
CC complementary strand of a polynucleotide which comprises a 5'-end
CC complementary strand of a polynucleotide which comprises a 5'-end
CC complementary strand of a polynucleotide which comprises a 1'-end sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence complementary to a
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC polynucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC particularly full-length cDNAs. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC cDNAs easily without any specialised methods. AAH03166 to AAH3628 and
CC cAAH13633 to AAH0368, all of which are used in the exemplification of the
CC consent inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer set
length cDN
diagnosis
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27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sets for synthesizing polynucleotides, particularly the 5602 full-cDNAs defined in the specification, and for the detection and/or sis of the abnormality of the proteins encoded by the full-length
                                           invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HELIX RES INST.
    2639 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO 12099; 2537pp +
    620 A; 706 C; 760 G;
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T, Wakamatsu
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Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Listing; English
    553 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito K,
C, Otsuki
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	Q E	1049 GTCCCTGTGTCCTACCTGCCGCTGTCCCGTGGAGCGGATCTGTAAAAACCACATCCTCA 1108
	P 29	989 GTTTGCAGCCCTGCATGCACACGTTCTGCGCGGCTTGCTACTCGGGCTGGATGGA
2117 TGGAGGTGAAGAGAGGTGTTTTTAAAATACAGAGACAAGCACGTCAAGGTGTTTTCACA	Db Qy	GTTTGCAGCCCTGCATGCACACGTTCTGCGGGGCTTGCTACTCGGGGCTGGATGGA
2057 TCTGTGAACAAGGTTCAAAAACTAAGCATCCAGAGGCCCTGAGCAGCTTTCAGCAC 	B Q	ACAAGATGGAGGAGACGCTGACATGCATCATCTGCCAGGACCTGCTGCACGACTGCTGCACATCTGCTGCAGACCTGCTGCACGACTGCTGACATCATCTTGCCAGGACCTGCTGCACGACCTGCTGCACGACCTGCTGACGACCTGCTGACAACATCATCTATCAACAACAACAACAACAACAACAACA
1997 ACTGGGGCCGTAACTGCCGCACTCAGGTGAAAGCTCACCACGCCATGAAATTCAATCATA 	Qy Db	GCTAGAAATGCCCAAACCGTCCACGAGGACGTCAGAGCAGCGGCTGGGAAGCCAG
1937 ATCGGCAGAACATTCCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCT	Db Qy	
1877 GAGACACCGTTCTGTGTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGT	D Q	797 ACAGAAAGACTGCGTCCTTTTCGTCGTTGGAACCCCAGGATCAGGAGGATTTGGAGCCCG 856
1817 CCGAGAGCCTCGTGGCTCTCCAGCGGGAGTGTTTCTGCTGTCTGATTACAGAGTCACGG	Db Qy	737 AAGGAAGTGGTCCCTCTGTGGCAAGTGATGAAGTCTCCAGCTTTTGCCTCAGCTCTCCCAG 796
1757 AGTCAGACATCCTGAAGAATTACCTGGCAACCAGAGGTTTGACATGGAAAAACATGTTGA 	B &	6 7
1697 TITGTGAGCTCAACCTGGGTGACAAGTGTCTGGACGGCGTGCTGAACAACAACAGCTACG 	Db Qy	617 AGCCATCAACATCGACGTCAGACCTCTTCCCCACAGCCTCGGCCTCTTCCACGGAGCCTT 676
1637 CTTTCTGCCACCTGTACTGGGGCTGCACCCGGACCGGCTGCTACGGCTGCCTGGCCCGT	Db Qy	557 GGGCCGATCCCCGGGTCCCTCCGTCGCCCGCCACTCAGGTGTGCTTTGAGGAACCAC 616
1577 GAGCGGAGCGCAGCAGGACCCGCGTGTCGCCCTCAGCAGTGTGCGGTCTGCCTGC	dp Vy	CTAACAAGGAAAATGTGTTCCATGGGACCAAAGATACCTCAGGTGCAGGTGCAGGGCGAG
1517 GCCCTCTGCAAGGAAGCCACGCCCTGTGCACCTGCTGCTTCCAGCCCCATGCCCGACCGGA 	D Q	437 TGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGACAAGAATCCTTTGAAG 496
1457 CCCTGGGGGATGCACCCTCCACGTCCGTCAGCCTGACGACAGCAGTCCAGGATTACCTGT	D QQ	377 CTTTACAGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAACCGGAACACAACG 436
ନ୍ସ=ନ	дь .ç	317 ATACCAGCACCAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCC 376
g=9	D 5	257 TCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGGTCAGGTGACACTGGAAG 316
	S B &	197 GGGAGTGGACCATCGGGCGGAGACGAGGTTGCGACCTTTCCTTCC
	? ₽ 4	137 GGGGACGGCTCCTGCGTCTGGGCGCGGAAGGAGGCCGAACGTCCTCCTGAGGAAGC 196
1109 ACAACCTCGTGGAAGCATACCTCATCCAGCATCCAGACAAGAGTCGCAGTGAAGAAGAAGATG	O D	

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27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises
(a) an oligo-dT primer and an oligonucleotide complementary to the
                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 fullength cDNAs defined in the specification, and for the detection and/or length cDNAs defined in the specification, and for the detection and/or length of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                      28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                                                           EP1074617-A2
                                                                                                                                                                                                                                                                                              Human; primer;
                                                                                                                                                                                                                                                                                                                Human cDNA sequence
                                                                                                                                                                                                                                                                                                                                   26-JUN-2001
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, Sugiyama
                                                                                                                                                HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGCGGCCGTCCCGCGAGAGGGGCAGTTTTGCTCTTTTGTACATTTTCCGAAACTACA
                                     f
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                                   NO 12127; 2537pp +
                                                                                                                   Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                     CDNA;
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                                                                                                                                                                                                                                                                                                                                  entry)
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                                                                                                                   Hayashi K, !
A, Nagai K,
                                    Sequence Listing;
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C, Otsuki
                                    English
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                                                                                                                              Yamamoto
                                                                                                                                                                                                                                                                                              therapy;
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Best Local Similarity
Matches 2454; Conserv
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CC complementary strand of a polynucleotide which comprises one of the 5602 CC nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination cf an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a complementary strand of a polynucleotide which comprises a 5'-end complementary to a complementary the complementary and in the complementary and in the complementary and in the complementary and in the full-length cDNAs. The primers are also useful for the complementary and analysis of the shormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and complementary invention and acid sequences; and AAH13629 to AAH13632 represent conjugation of the complementary invention.
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3138 BP; 738 A; 824 C; 873 G; 703 T; 0 U; 0 Other;

84.4%; 93.0%;

DB

Length 3138;

481 421 447 361 387 301 241 327 267 181 207 121 147 61 27 CCCGATGGAGCGGCCCGAGGAAGGCAAGCAGTCGCCGCCGCCGCAGCCCTGGGGACGGCC CAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCCTTTACAGAC CAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCTTTACAGAC CATCGGGCGAGACGATGCCAACCTTTCCCCCAGCAATAAACTGGTCTCTGGAGA CATCGGGCGGAGACGAGGTTGCGACCTTTCCCTCCCAGCAATAAACTGGTCTCTGGAGA CTCTTGACAGCGGCGGCGGCGCGCGGCCCGGTTCCGGGTTCCGGCGCGCGGGGCGGGGATGTGAAT GCGAGAGCGTTCCTCCAGTTGTGGGTCTGGGGGTGGTCGCCATCTCCCCCTAAAGGAAGTGG CTGTGTTGCCCAGGCTGGTCTAAAACTCCTGGGATCAAGT------ANATGTGTTCCATGGGACCANAGATACCTCAGGTGCAGGTGCAGGGCGAGGGGCCGATCC CTATGAATCTTTAAGTGAAAAGCAAGGCATGACACAAGAATCCTTTGAGATGGTGCCTTG CTATGAATCTTTAAGTGAAAAGCAAGGCATGACACAAGAATCCTTTGAAGCTAACAAGGA TGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAACCGGGAACACAACGTGGCATACCT TGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAACCGGAACACAACGTGGCATACCT CCTGCGTCTGGGCGCGAGGAGGGGAGCCGCACGTCCTCCTGAGGAAGCGGGAGTGGAC CCTGCGTCTGGGCGCGGAGGAGGCGAGCCGCACGTCCTCCTGAGGAAGCGGGAGTGGAC ATCGACGTCAGACCTCTTCCCCACAGCCTCGGCCTCTTCCACGGAGCCTTCTCCTGCAGG Conservative -GATCCTCCCACCTTGGCCTCCCAAAGTATTGTGATTACA-٥, Score 2262.4; Pred. No. 0; 0; Mismatches 61; Indels 125; Gaps 746 559 686 626 566 180 146 86 597 506 446 360 386 300 326 240 266 206 120 60 420

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ABN59646 standard; cDNA; 3181 ВP

ABN59646

28-JUN-2002 (first entry)

Novel human coding sequence SEQ ID NO: 57.

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Best Local Similarity
Matches 1995; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1995 BP; 465 A; 563 C; 580 G; 387 T; 0 U; 0 Other;
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             TGTAGAATTGTAGTGGATGAAAAATCAGGTCAGGTGACACTGGAAGATACCAGCACCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2448
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DE Human polynucleotide
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W Human; cytokine; cel
KW Human; cytokine; cel
KW vaccine; peptide the
KW tissue growth factor
KW nervous system disor
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                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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production of other cytokines in other cell populations. The polynuclectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a CC pathological condition. Antibodies to the proteins can also be used in CC alleviating symptoms associated with the disorders and in diagnostic conditions. The condition or susceptibility to a communoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune cC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac nervous system disorders e.g. alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, can dmany other disorders listed in the specification. The polypeptides CC can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used capabilities, fat content, lipid, process, cardiac, vitamins, cmissient, in the contents. The present content, lipid, process, cardiac, vitamins, many content, lipid, process, cardiac, vitamins, capabilities, fat content, lipid, process, cardiac, and contents. The present contents and other nutritional components. The present content distance and content form part of the invention. Note: The sequence data for this patent did not form part of the printed
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Best Local
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TCCAGCCCATGCCCGACCGGAGAGAGAGCGGAGCAGGA-CCCGCGTGTCGCCCCTCAG
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Human; gene; ds; neural disorder; immune system disorder; renal disorder muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic. disorder;

2000US-0179065P 2001US-00764864

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The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. ansal vestibulitis, nasal polyps and sinusitis), reproductive disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendictis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences AEX73173-ABX74167 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 1267; Conserv
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01-NOV-2000;
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                                                AGAATGAACCGGAACACAACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCA
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6; Mismatches
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TCCAGCCCATGCCCGACCGGAGAGCGGAGCGAGCAGGA-CCCGCGTGTCGCCCCTCAG
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                                                 CAGCAGTCCAGGATTACGTGTGCCCTCTGCAAGGAAGCCACGCCCTGTGCACCTGCTGCT
                                                                                                TGCTGCAGCCCAAAGTCAGGCGGTCTTTTTCTGATGAAGAAGGGAGTTCAGAGGACCTGC
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                                                                                                                              Query Match
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Matches 890
                                                                                                                                                                                   The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                   Sequence 2186 BP; 493 A; 555 C; 539 G;
                                                                                                                                                                                                                                                              New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2001; 2001JP-00328381.
24-JAN-2002; 2002US-0350435P.
                                                                                                                                                                                                                                                Claim 1;
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o J, Isono Y,
Yoshikawa T,
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                                                                                                   AGAATTACCTGGCAACCAGAGGTTTGACATGGAAAAACATGTTGACCGAGAGCCTCGTGG
            GTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTATCAGTATCGGCAGAACATTC
                          GTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGCAGAACATTC 1951
                                                           CTCTCCAGCGGGGAGTGTTTCTGCTGTCTGATTACAGAGTCACGGGAGACACCGTTCTGT
                                                                                       AGAATTACCTGGCAACCAGAGGTCTGACATGGAAAAACATGTTGACCGAGAGCCTCGTGG
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disease; gene; ss.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
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07-FEB-2001
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28-JUL-2000;
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CC (a) an oligo-dT primer and an oligonucleotide complementary to the

CC complementary strand of a polynucleotide which comprises one of the 5602

CC nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprises a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of

CC oligonucleotide which comprises as real sequence, where the

CC specification. The primer sets can be used in antisense therapy and in

CC gene therapy. The primers are useful for synthesising polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers alre also useful for the

CC DNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC CAAH13633 to AAH19742 represent human cDNA sequences; AAB92446 to AAH35893

CC represent human amino acid sequences; and AAH13629 to AAH13632 represent

CC construction of the
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length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
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, Sugiyama
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Wakamatsu A, Nagai K,
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
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T, Wakamatsu
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CC The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC complementary strand of a polynucleotides; or (b) a combination
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC complementary strand of a polynucleotide which comprises a 5'-end
CC complementary strand of a polynucleotide which comprises a 5'-end
CC equence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC conjugate of the sequence of sequence, where the
CC conjugate of the sequence of sequence, where the
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primers are useful for synthesising polynucleotides,
CC particularly full-length CDNAs. The primers are also useful for the
CC specification and/or diagnosis of the subnormality of the proteins encoded by
CC cDNAs easily without any specialised methods. AAH303166 to AAH3528 and
CC CANAS333 to AAH3742 represent human CDNA sequences; ABB92486 to AAB95893
CC represent human amino acid sequences; and AAH33629 to AAH33632 represent
CC CREENT invention
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                                             ATCGACGTCAGACCTCTTCCCCCACAGCCTCGGCCTCTTCCACGGAGCCTTCTCCTGCAGG
                                                                                                                                          CTATGAATCTTTAAGTGAAAAGCAAGGCATGACACAAGAATCCTTTGAGATGGTGCCTTG
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Pred. No. 7.1e-130;
0; Mismatches 62;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                cerebral ischaemia; angiogenesis; nervous system disorder; Alzhaimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                     cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
                                                                                                                                                                                 18-APR-2000;
19-MAY-2000;
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17-MAR-2000;
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The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used CC in diagnosing a pathological condition or susceptibility to a CC pathological condition. Antibodies to the proteins can also be used in CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. carests, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, CC nervous system disorders e.g. Alzheimer's disease, infections caused by acteria, viruses and fungi and ocular disorders e.g. corneal infection, CC and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, CC transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used contact or preservative to increase or decrease storage
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Best Local Similarity
                                             Human; gene, ds; neural disorder; immune system disorder; renal disorder muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
                                                                                                                                                                                                                                                                Human novel
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Claim 1; SEQ ID

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483; 402pp; English

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13-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
17-NOV-2000;
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22-AUG-20000

30-AUG-20000

01-SEP-20000

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05-SEP-20000

05-SEP-20000

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22-SEP-20000

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29-SEP-20000
                     New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular o
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14-AUG-2000;
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The invention relates to human novel polypeptides and their associated CC polynucleotides. The polypeptides and polynucleotides are useful in gene CC therapy for treating, inhibiting or preventing neural disorders, immune CC system disorders (e.g. systemic lupus crythematosus, rheumatoid arthritis cand multiple sclerosis), muscular disorders, respiratory diseases (e.g. cand multiple sclerosis), muscular disorders, respiratory diseases (e.g. cand multiple sclerosis), muscular disorders, respiratory diseases (e.g. cand vestibulitis, nasal polyps and sinusitis), respiratory diseases (e.g. cardiovascular disorders (e.g. disorders (e.g. disorders (e.g. disorders (e.g. hodgkin's disease and capendicitis), allergic reactions and conditions (e.g. asthma), blood crelated disorders (e.g. thrombosis, atherosclerosis and myocardial CC infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent xxx
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Best Local &
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CCACCTGTACTGGGGCTGCACCCGGACCGGCTGCTACGGCTGCCTGGCCCCGTTTTG 1700
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92.5%;
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Pred. No. 9.8e-119;
7; Mismatches 13;
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immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; mostropic; antiparkinsonian; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; altergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Albeimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                WPI; 2000-317938/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed sequence tag; EST; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; mouse; chicken; rat; secreted expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:911
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                                                                                                                                                                                                                                                                                                                                                                                Evans
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Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders us disorders disorders.

Claim 1; Page 437; 803pp; English.

CC carebroprotective; anticonvulsant; and antidepressant. The SESTs can bave a cange of activities depending on the correct togs (RESTs), isolated from human, mouse, chicken and rat tissue CC sources. The SESTs can have a range of activities depending on the CL issues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analyesic; chemostatic; thrombolytic; antifilammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiulcer; costeopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic; cc cerebroprotective; anticonvulsant; and antidepressant. The SESTs can be cc used for gene therapy and in vaccines. The SESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA cmolecules which correspond to the SESTs. Proteins encoded by the SESTs care useful in assays for determining biological activity and raising care useful assays for determining biological activity and raising care useful assays for determining biological activity and raising care useful assays for determining biological activity and raising care useful assays, insulin dependent diabetes), allergic conditions (Maltiple sclerosis, insulin dependent diabetes), allergic conditions (Casthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and pooriasis. AAA45226 to AAA45931 represent linker variants which are given in the transfer of the process in the company of the process in t the exemplification of the present invention

Sequence 575 BP; 124 A; 168 C; 165 G; 118 T; 0 U; 0 Other;

Query Match Best Local Similarity Matches 532; Conservative 18.5%; 0 Score 495.8; DB 3; Pred. No. 6e-109; Mismatches 7; Indels 22; Gaps

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863	AGAAAATGAGAGGAGATGGGGACCTTGACCTGAACGGG 900
250	AGAAAATGAGAGGAGAACACATCCCTTTCTCCTGTAGATGGGGACCTTGACCTGAACGCG 309
901	CAGTTGTTGGTCGCACAACCGGGTAGAAATGCCCAAAACCGTCCACGAGGACGTCAGAGCA 960
310	CAGTTGTTGGTCGCACAACCGCGTAGAAATGCCCAAACCGTCCACGAGGACGTCAGAGCA 369
961	GCGGCTGGGAAGCCAGACAAGATGGAGAGACGCTGACATGCATCATCTGCCAGGACCTG 1020
370	GCGGCTGGGAAGCCAGACAAGATGGAGGAGACGCTGACATGCATCTCTGCCAGGACCTG 429
1021	CTGCACGACTGCGTGAGTTTGCAGCCCTGCATGCACACGTTCTGCGCGGGCTTGCTACTCG 1080
430	CTGCACGACTGCGTGAGTTTGCAGCCCTGCATGCACACGTTCTGCGCGGGCTTGCTACTCG 489
1081	GGCTGGATGGAGCGCTCGTCCCTGTGTCCTACCTGCCGCTGTCCCGTGGAGCGGATCTGT 1140
490	GGCTGGATGGAGCGCTCGTCCCTGTGTCCTACCTGCCGCTGTCCCGTGGAGCGGATCTGT 549
1141	AAAAACCACATCCTCAACAAC 1161
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Search completed: January 15, 2005, 00:57:44 Job time : 1249 secs

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DEFINITION
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Martineried/Germany) within the CDNA sequencing consortium of the German Genome Project. This clone (DKFZp434N2420) is available at the RZPD beutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp434N2420 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2297)
Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Schaipp, A.,
Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                       Submitted (03-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                                                                                                                                                                                     Direct Submission
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AL137561
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/codon_start=1
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                                                        AACATTCCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGGGC
                                                                               AACATTCCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGGGC
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/protein id="CAB70812.1"
/db_xref="G1:6808266"
/translation="VEAYLIQHPDKSRSEEDVQSMDARNKITQDMLQPKVRRSFSDEE
GSSEDLLELSDVDSESSDISQPYVVCRQCPEYRRQAAQPPHCPAPEGEPGAPQALGDA
STSVSLITAVQDYVCPLQGSHALCTCCTQPMEDRRAERQDEPKAPQQCAVCLQPFC
HLYMGCTRTGCYGCLAPFCELMLGMCKLDGVLKNNNSYSEDILKNYLATRGLTWKNMLT
ESLVALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASELPVAVTSRPD
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                 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                AK077629 3146 bp mRNA linear HTC 03-API Mus musculus 8 days embryo whole body CDNA, RIKEN full-length enriched library, clone:5730484M20 product:similar to CELL CYC CHECKPOINT PROTEIN CHFR [Homo sapiens], full insert sequence.
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Mammalia; Eutheria;
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16 APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIXEN Genomic Sciences Center (GSC), RIXEN Yokohama Institute; 1-7-22 Suehino-cho, Tsurumi-ku, Yokohama, Kanagawa 20-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Analysis of the mouse transcriptome based on of 60,770 full-length CDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepare mouse tissues.
Please visit our web site for further details.
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6 (bases 1 to 3146)
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URL:http://fantom.gsc.riken.jp/.
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                                                                  /note="unnamed protein product; putative similar to CELL CYCLE CHECKPOINT PROTEIN CHFR [Homo sapiens] (SPTR[O9NRT4, evidence: FASTY, 81.7%ID, 100%length, match=1989)"
                                                                                                                                                                                                         /clone="5730484M20"
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                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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                                                                                                                                                                                       /dev_stage="8 days embryo"
                                                                                                                                                                                                                                                                                             db_xref="FANTOM_DB:5730484M20"
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/note="putative"

Similarity CCGCAATGTCTCTTGACAGCGGCGGCGGCG-----CAGCCGGTTCCGGGGTTCGGCGCGG GCCCTGGGGACGGCTCCTGCGTCTGGGCGCGGAGGAGGGCGAGGCCGCACGTCCTCAAG 191 ACCCTGGGGGGAGGCTTCTTCGTCTAGGCGCGCAGAGGAGGACCAAACCCCAGATCCTTCTTTG GGCGTGGGATGTGAGTCCTATGGAGCTACACGGGGAAGAGCAGCCGCCGCCGCCGCAGGA GGCGGGGATGTGAATCCCGATGGAGCGGCCCGAGGAAGGCAAGCAGTCGCCGCCGCCGCA 131 GAAACGCGAGTGGACCATCGGAAGGAGGAGAGGCTGTGACCTCTTTTCCCCCAGCAATAA CCGAGATGTCTGTTGACAGCGGTGGCGGCGACTGTAAGGCCGGTTCCGGGATCCGCGCAG Conservative 54.7%; <u>.</u>, Score 1464.6; Pred. No. 0; Mismatches 634; Indels DB 3; Length 52; 249 189 69

ATGCCCTTTACAGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAACCGGAACA TTACCCTTTACATAGCGGGGATATCATCTATTTGGTGTACAGGAAGAATGAGCCAGAACA ACCACAGCCATCAACATCGACGTCAGACCTCTTCCCCACAGCCTCGGCCTCTTCCACGGA 671 GGAAGATACCAGCACCAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGAAGCAGAC ACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGGTCAGGTGACACT CATCTCCCCAAAAGGACGCAGTTCACTTGTTGCAAATGGCGAACTCTCTAGCCTTTCTCC CATCTCCCCTAAAGGAAGTGGTCCCTCTGTGGCAAGTGAAGTCTCCAGCTTTGCCTC GCCAGAGCTGACCTCTGCAGGGCAAAAGCATTCTTCTAGCTCTGGACCTGGGAACACAAG GCC----TTCTCCTGCAGGGCGAGAGCGTTCCTCCAGTTGTGGGTCTGGGGGTGGTGG GCAGGGTGATGATCCCCAGGTTCCACTATTGTCACCCATGGCTCAGACATGCTTAGAGGA TGAAGCCAATAAGGAAAATATGTTCCATGTGACCAAAGATTGCT-----CAGGTCCAGG TGAAGCTAACAAGGAAAATGTGTTCCATGGGACCAAAGATACCTCAGGTGCAGGTGCAGG CAATGTGGCATACCTCTATGAATCTTTAAGTGGCAAACAGAGCTTAACTCAAGACTCCCT CAACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGACACAAGAATCCTT GGAAGACACCAGCACCAATGGAACAGTGATCAATAAGCTGCAAGTTGTTAAGAAGCAGAC ACTGGTCTCTGGAGATCACTGTAAACTTACAGTGGATGAAATATCTGGTGAGGTGACACT 603 611 551 429 431 369 725 663 543 489 491 309 311

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CATTCTGTGAGCT PACGAGTCAGACAT	561 GCCTGACCGGAGAGCTGAACG 626 CTGCCTGCAGCCTTTCTGCCA 621 GTGCCTGCAGCCTTTTGCCA 621 GTGCCTGCAGCCTTTTGTGCA 686 CCTGGCCCCGTTTTTGTGAGCT	GCCCCACAGGCCCTGGGGGATGCACCCTCA 	326 AGACGTT 321 TGATGTC 386 TGAGTAC 381 TGAATAC	1206 TGAAGAAGATGTGCAAAGTATGGATGCCAGGAATAAAATCACTCAAGACATGCTG	086 GATGGAGCGCTCGTCCCTGTGTCCTACCTC	966 TGGGAAGCCAGACAAGATGGAGGAGACGCTGACA	4 AGTTTTCCAAG 6 TTTGGAGCCG 1 1 ATTGGAGCCTG 6 GTTGGTCGCAC 1 ATTAGTTTCAG
CAACCTGGGGACAAGTGCTTGGATGAGTGTTTTAACAA 1740 CCTGAAGAATTACCTGGCAACCAGAGGTTTGACATGGAA 1805		CTTTAAGTAGTTTTG	C 138 C 144	CAGCC CAACC CTGTC CTGTC	CCGCTGTCCCGTGGAGCGGATCTGTI	GACATGCATCAGCTGCCAGGACCTGCTGCA 1025	TTTGCTGG TGGGGACC TGGGGAAC TGGGGAAC

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	2633 TGTAGCACAAATACTATAATTTTACAAAATTGACTAAAATTAGGAATA 2685	2623 TGTAGCACAAATAATATAATTTATAATTTACAAATTGACAAAAAAAA	2573 TATTTTTTATTTTAATAAGTTTTGGTGCTTAGTCTTGTAATAAGATTTAAATATTAAAAAC 2632	2564 TATTTTTATTTTAATAGGTTTGGTGCTTA-TCTTCTAATAAGATTTAAATGTCACAAAC 2622	2513 TTTACAGCCTCCAGGGGTACATAGGATAGTCTCCTCTGGAAAGACACAGCCTTTTGTA 2572	2505 TTTACAGCCTACAGGACGT-ACACAATATCCTGCTGCTGCGGAAAACCACACACATTTTATC 2563	2453 CTCATAGGAAAAGTTGTCAGCTGTGTCAGACGCATTCTCCCGGAAGGAA	2447 TTTCAAGGGAAGGCAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAG 2504	2399 TIGIACTTTTGTATCTTTTCTACCTTGTACCTTGACTATGGTTAAAATGGGAAG 2452	2387 TIGCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAG 2446	2339 CTCCCTCCCACTGGACCGCTCTCCCCTCTGTGTGCTGAGGCAGTGACAGTGCAGGT 2398	2340ACGAAGCCTTTCTGTAACATGCGGCCGTCCCGCCGAGAGGGGCAGTT 2386	2279 GGGAGGCCTCCTGGCCACACCAGCCTTCTAGTCGGTGTAAGAGATCAGTAGACTGAGTT 2338	2286 GCCCGCCCTCCTGGTGAGCGCTGGGCAGGGCTCGTGGTGGCATCAGCAGCAGAG 2339	2220 ATTTTCCCTTTGTGGAGCGTCATCGTCAGTGACACACACCACGTGCCCCCAGTAAC-CT 2278	2226 CTCTTCTGTGGAGCTTTTTTACCCTCTGAGTGAGGCCCTCCCCAGAGCCCCCGGGGGCCGCA 2285	2160 GGCATTTTTACAGTTTTCCCTACGCAGCACTGGGGGTTCTGGTCAGGCACTGGGGTGTGG 2219	2166 GTGTTTTCACAGCCCCCTGAGGGAAGGGACGCAGGGTCTCCGACAGGTGCTCTGGGGTGA 2225	2101 AACAGTTACAGAGCA-CAGGAGGCAATGTTTTTTAAAAGGCCCCATACAAACACTTGAAG 2159	2106 GCTTTCAGCACTGGAGGTGAAGAGAGCGTGTTTTTAAAATACAGAGACAAGCAAG	2041 ATTCAATCACATCTGTGAGCAAACAAGGTTCAAGAACTGAATATTGGAAGAGACACGTGA 2100	2046 ATTCAATCATATCTGTGAACAGACAAGGTTCAAAAACTAAGCATCCAGAGGCCCTGAGCA 2105	1981 TCCTGACTGCTACTGGGGCCGTAACTGTCGCACTCAGGTGAAGGCTCACCATGCAATGAA 2040	1986 TCCTGACTGCTACTGGGGCCGTAACTGCCGCACTCAGGTGAAAGCTCACCACGCCATGAA 2045	1921 GACCTACCAGTATCGTCAGAACATTCCTGCTTCTGAGTTGCCAGTGACTGTAACATCCCG 1980	1926 GACCTATCAGTATCGGCAGAACATTCCTGCTTCCGAGTTGCCCAGTGGCCGTAACATCCCG 1985	1861 CAGAATCACTGGAAATACTGTGTGTTACTGCTGTGGTCTGCGTAGCTTCCGAGAGCT 1920	1866 CAGAGTCACGGGAGACACCGTTCTGTGTGTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCT 1925

REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE ORGANISM 1 Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning

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LOCUS DEFINITION AKO48930

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AKO48930

Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230082M18 product:similar to CELL CYCLE CHECKPOINT PROTEIN CHFR [Homo sapiens], full insert sequence.

AKO48930

AKO48930.1 G:26093209

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (bridata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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                                                                                                                                          prepare mouse tissues.
Please visit our web site for further details.
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                  Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohi Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9216)

URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)

cDNA ilbrary was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken.
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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/db_xref="taxon:10090"
                                                                                                organism="Mus musculus"
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/note="similar to CELL CYCLE CHE sapiens] (SPTR|Q9NRT4, evidence: 100%length, match=1989)"
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Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation
                                                                                                                division of Invitrogen.
Location/Qualifiers
1. .2412
                                                                                                                                                                   Submitted (20-UII-2004) Genoscope - Centre National de Sequencage: BP 1919106 EVRY Cedex - FRANCE (B-mail: seqref@genoscope.cns.fr)
BP 19106 EVRY Cedex - FRANCE (B-mail: seqref@genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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Mammalla; Eutheria; Primates;
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/mol_type="mRNA"
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invirogen.
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Li.W.B., Gruber, C., Jessee, J. and Polayes, D.
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    Conservative
                                                                                                       /tissue_type="FETAL BRAIN"
/dev stage="fetal"
/dev stage="fetal"
/clone lib="Homo sapiens FETAL BRAIN"
/clone lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; lst strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                    clone="CS0DF031YA23"
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                      34.2%;
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10 sapiens FETAL BRAIN Homo sapiens cDNA clone
3-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates; C.
1 (bases 1 to 1118)
Li,W.B., Gruber,C., Jessee,J. au
Full-length cDNA libraries and unpublished (2001)
On Feb 15, 2001 this sequence v.
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segret@genoscope.cns.fr Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence belongs to sequence cluster 6792.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODF031AA12NP1&c=6792.r. Location/Qualifiers
GTGAACAGACAAGGTTCAAAAACTAAGCATCCAGAGGCCCTGAGCAGCTTTCAGCACTGG
                                                                           GGGGCCGTAACTGCCGCACTCAGGTGAAAGCTCACCACGCCATGAAATTCAATCATATCT
                                                       GGGGCCGTAACTGCCGCACTCAGGTGAAAGCTCACCACGCCATGAAATTCAATCATATCT
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECGRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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/db_xref="taxon:9606"
/clone="CSODF031YA23"
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/dev_stage="fetal"
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Pred. No. 1.5e-224;
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Length Indels

1118; 6;

Gaps

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1759

884

1699 1001

944

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764

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Gaps

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REFERENCE
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B76 bp mRNA linear EST 16-AUG-2002
AGENCOURT 8681666 NIH MGC_43 Homo sapiens cDNA clone IMAGE:6376937
5', mRNA sequence.
BQ876252
                                                                                                 CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2559 row: o column: 18
High quality sequence stop: 678.
Location/Qualifiers
                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                (bases 1 to 876)
/organism="Homo sapiens"
/mol type="maNn;
/db_xref="reaxon:9606"
/clone="IMAGE:6376937"
/tissue_type="normal pigmented retinal epithelium"
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     -GCCGTAACTGCCGCACTCAGGTGAAAGCTCACCACGC 2039
                                                      AGAACATTCCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGG
                                                                                                    CCGTTCTGTGTTACTGCTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGC
                                                                                                                         CCGTTCTGTGTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGC
                                                                                                                                                                                                 CTCGTGGCTCTCCAGCGGGGAGTCTTTCTGCTGTCTGATTACAGAGTCACGGG--AGACA
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                                   AGAACATTCCTGCTTCCGAGNTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGG
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/clone lib="NIH_MGC_43"
/clone lib="NIH_MGC_43"
/note="Cryan: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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98.3%;
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Pred. No. 1.7e-201;
0; Mismatches 9;
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13467 row: e column: 18
High quality sequence stop: 697.
Location/Qualifiers
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National Institutes of Health,
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 921)
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EST.
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                         AAGGGACGCAGGGTCTCCGACAGGTGCTCTGGGGGTGACTCTTCTGTGGAGCTTTTTTACCC
                                                                GAGCGTGTTTTTAAAATACAGAGACAAGCACGTCAAGGTGTTTTCACAGCCCCCTGAGGG
                                                                                                    GAGCGTGTTTTTAAAATACAGAGACAAGCACGTCAAGGTGTTTTCACAGCCCCCTGAGGG
                                                                                                                                                                  CAAGGTTCAAAAACTAAGCATCCAGAGGCCCCTGAGCAGCTTTCAGCACTGGAGGTGAAGA 2128
                                                                                                                                                                                                                          ACTGCCGCACTCAGGTGAAAGCTCACCACCGCCATGAAATTCAATCATATCTGTGAACAGA
                                                                                                                                                                                                                                                                        TTCCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGGGCCGTA
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                                                                                                                                                                                                                                                                                                                                           TGTGTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGCAGAACA
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                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="IMAGE:6143609"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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SOURCE
ORGANISM
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1 (bases 1 to 870)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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Mammalia; Eutheria; Primates;
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BQ215731
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Plate: LLAM13325 row:
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/clone="IMAGE:6059147"
/tissue_type="large_cell carcinoma"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NH1M GC_68"
/clone_lib="NHH MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo of Steeles (primer: size 1.8 kb. Library constructed by Library const
                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Query Match

28.6%;

Score 765.4;

DB 5;

Length 870;

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RESULT 10
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5', mRNA sequence.
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EST.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 992)
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Arrayed by: The I.M.A.G.R. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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                                              GCGTGAGTTTGCAGCCCTGCATGCACACGTTCTGCGGGCTTGCTACTCGGGCTGGATGG
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                         GCGTGAGTTTGCAGCCCTGCATGCACACGTTCTGCGCGCGTTGCTACTCGGGCTGGATGG
                                                                                                                                           AGCCAGACAAGATGGAGAGAGACGCTGACATGCATCATCTGCCAGGACCTGCTGCACGACT
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Location/Qualifiers
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/clone="IMAGE:8806133"
/tissue_type="epidermoid carcinoma, cell line"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_101"
/clone_lib="NIH MGC_101"
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2: EcoRiched: pote-2:
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Pred. No. 7.8e-185;
0; Mismatches 25;
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Query Match 28.3%; Score 757.6; DB 6; Length 877; Best Local Similarity 96.9%; Pred. No. 9.6e-185; Matches 772; Conservative 0; Mismatches 25; Indels 0; Gaps 0; Qy 1527 AGGAAGCCACGCCCTGTGCACCTGCTGCTTCCAGCCCATGCCCGACCGGAGAGCGGAGCG 1586	/organism="Homo sapiens" /mol_type="mRNA" /db xref="taxon:9606" /clone="IMAGE:30383176" /lab_host="PH10B-Ton A (T1 and T5 phage resistances)" /clone_lib="NIH_MGC_180" /note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: NotI; Site_2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."	Tissue Procurement: Dr. Michael Brownstein cDNA Library Preparation: Invitrogen Corp cDNA Library Preparation: Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Plate: NDAM446 row: j column: 17 High quality sequence stop: 660. FEATURES Location/Qualifiers 1.877	KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE 1 (bases 1 to 877) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov	1387 GAGTAC 138	Qy 1091 AGCGCTCGTCCTGTGTCCTACCTGCCGCTGTCCCGTGGAGCGGATCTGTAAAAACCACA 1150 bb 541 AGCGCTCGTCCCTGTGTCCTACCTGCGCTGTCCCGTGGAGCGGATCTGTAAAAACCACA 600 Qy 1151 TCCTCAACAACCCTCGTGGAAGCATACCACATCCAGACCAAGAGAGCAAGAGTGAAG 1210 Qy 1211 AAGATGTGCAAAGCTATGGAAGCATACCTCATCCAGCACTCAAGAAGTCCCAGAGTGAAG 660 Qy 1211 AAGATGTGCAAAGTATGGAATGCAGGAATAAAATCACTCAAGAAGAGTCGCAGTGAAG 1269
Mammalia; Metazoa; Chordara; Craniara; Vertebrara; kuteleoscomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 910) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE Mational Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D.	SULT 12 148471 CUS EINITION AGENCOURT 8675647 NIH MGC 40 Homo sapiens cDNA clond clo	Qy 2187 GGAAGGACGCAGGTCTCCGACAGGTGCTCTGGGGTGACTCTTCTGTGGAGCTTTTTAC 2246	CY 2007 TAACTICCCGCACTCAGGTGAAAGCTCACGCCGTGAAATTCAATTCATATCTGTGGACA 2066	304 1887 364 1947 424	

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                      CAACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGACACAAGAATCCTT
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/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
/inte="Cronel; cDnA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC_Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.plate: LLCM1300 row: a column: 18
High quality sequence stop: 775.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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602458365F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4580633
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/tissue_type="retinoblastoma"
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/clone_lib="NH10B (phage-resistant)"
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/clone_lib="NH1MGC_16"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Query Match 27.2%; Best Local Similarity 95.8%; Matches 779; Conservative

Score 727.4; DB 4; Pred. No. 6.4e-177; 0; Mismatches 31;

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BQ936072
BQ936072.1 GI:22351455
EST.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCND546 row: p column: 17
High quality sequence stop: 630.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
GCCCGCCACTCAGGTGTGCTTTGAGGAACCACAGCCATCAACATCGACGTCAGACCTCTT
                                                                                         CAAAGATACCTCAGGTGCAGGTGCAGGGGCGAGGGGCCGATCCCCGGGGTCCCTCCGTCGTC
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                                                                                                                                                 AAAGCAAGGCATGACAAGAATCCTTT------
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/lab host="DHIOB (phage resistant)"
/clone lib="NIH MCC_18"
/clone lib="NIH MCC_18"
/clone lib="NIH MCC_18"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: RocRI; cDNA made by oligo-dT prining. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:6371968"
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REFERENCE AUTHORS TITLE

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RESULT 14 BQ936072 LOCUS

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KEYWORDS

ORIGIN	FEATURES	ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 15 BQ924736 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE	B & B & B	Q B Q B Q B
/or /mc /cl /cl /la /la /nc Ecc Ent GGC Int Int Sug Sug NIII	Tissue Procurement: DCTD/DTP/Gazdar Tissue Procurement: DCTD/DTP/Gazdar CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2552 row: i column: 23 High quality sequence stop: 629. Location/Qualifiers Ge 1. 938	Homo BE Eukaryo Mammall 1 (bas NIH-MG NIH-MG NATion Unpubl	BQ924736 BQ924736 AGENCOURT 8853777 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6374110 5', mRNA sequence. BQ924736 BQ924736 BQ924736 BC924736.1 GI:22339767 EST. Homo sapiens (human)	745 Trigáhácicichágáriccagánaígáriritógágictógránásásánánáránnágánásárig 804 881 GGGACCTTGACCTGAACGGCAGTTGTTGGTCGCACAACCGCGTAGAATGCCCA 935	505 GCCCGCCACTCAGGTGTGCTTTGAGGAACCACAGCCATCAACATCGACGTCAGACCTCTT 564 645 CCCCACAGCCTCGGCCTCTTCCACGGAGCCTTCTCCTGCAGGGCGAGAGCGTTCCTCCAGG 565 CCCCACAGCCTCGGCCTCTTCCACGGAGCCTTCTCCTGCAGGGCGAGAGCGTTCCTCCAG 704 565 CCCCACAGCCTCGGCTTCTCCCACGGAGCCTTCTCCTGCAGGGCGAGAGCGTTCCTCCAG 624 705 TTGTGGGTCT-GGGGGTGGTGGCATCTCCCCTAAAGGAAGTTGGTCCTCTGTGGCAAGTG 763
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Search completed: January 15, 2005, 06:17:46 Job time: 8064 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Perfect score:
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                                                                                                  seq length: 0
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US-09-252-991A-2607
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US-09-39-3-32C-8
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PCT-US-6-02331-9
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                        Sequence 14, Appl Sequence 16556, A Sequence 13, Appl Sequence 25, Appl Sequence 25, Appli Sequence 25, Appli Sequence 27, Appli Sequence 27, Appli Sequence 321, Appli Sequence 2007, Appli Sequence 2445, App Sequence 2607, Appli Sequence 62, Appli Sequence 1, Appli Sequence 1, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 14, Appli Sequence 9, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 112, Appli Sequence 243, Appli Sequence 183, Appli Sequence 181, App
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Query Match
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                              IMMEDIATE SOURCE:
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Sequence 128, App	Sequence 128, App	Sequence 128, App	Sequence 31, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 45, Appl	Sequence 45, Appl	Sequence 101, App	Sequence 41, Appl	6	Sequence 4, Appli	Sequence 15639, A	Sequence 1, Appli	Sequence 178, App	Sequence 81, Appl	Sequence 10, Appl

ALIGNMENTS

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Sequence 14, Application US/08232463 Patent No. 5670367
                                          COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Vei CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463 FILING DATE: CLASSIFICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: US/07/935,313 FILING DATE: APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNSY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 ITELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEPAX: (703)838-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
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Best Local Similarity
Matches 57; Conserv
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Patent No. 6639063
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ESTs and Encoded Human Proteins FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dumas Milne Edwards, APPLICANT: Jobert, S.
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     1768
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                                                                                                         GGSCMMYTKRMMRRMCCCCMRRRSMRRRRMCMWKGSYTYCYKSSSMMCMARRWKRARGKK 235
                                                                                                                                                                                                                                                   SGRAMCCYYYKKKGSCSRAMCCCCYTYCYKSCCSSYKGSYTTKRAMMWKRRSCYTYSRRR 115
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   CTGAAGAATTACCTGGCAACCAGAGGTTTGACATGGAAAAACATGTTGACCGAGAGCCTC 1827
                                    RMCCYTKGGGRMMRKYCCMRKKGRRACCTGTTCACCTGCCGTGTCTGCCAGAAGGCCTTC
                                                                       AACCTGGGTGACAAGTGTCTGGACGGCGTGCTGAACAACAACAGCTACGAGTCAGACATC
                                                                                                                                            MYYYWRSYWMMRSMWKGSCCCCSGGSCYKKKKKGKKGSCCMRSYWMCCYYYKRARRMWWK 175
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US-09-807-258-13
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Best Local Similarity 49.4%;
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Patent No. 6063570
GENERAL INFORMATION:
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LENGTH: 1759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                       APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'REEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-T
TITLE OF INVENTION: ENZYMES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. DU PONT DE NEMOURS AND CO
STREET: 1007 MARKET STREET
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/807,258
CURRENT FILING DATE: 2001-06-11
PRIOR PPLICATION NUMBER: 60/104,376
PRIOR FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Arthropod Protein Disulfide Isomerases
FILE REFERENCE: BB-1253 PCT
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50
COMPUTER: IBM PC COMPATIBLE
                                                                                          STATE:
                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1694
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                                                         19898
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                                                                                        DELAWARE
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                                                                      UNITED STATES
                                                                                                                                                                                               DANIEL SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
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                    3.50 INCH
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Pred. No. 0.11;
0; Mismatches 122;
                                                                       AMERICA
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                                                                                                                                            COMPANY
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Gaps

2558 1633

CURRENT APPLICATION DATA:

OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95 SOFTWARE: MICROSOFT WORD VERSION 7.0A

APPLICATION NUMBER: US/08/924,747

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US-09-247-373B-25
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                                                                             , TYPE: DNA
, ORGANISM: SOYBEAN
US-09-247-373B-25
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                                                                                                                             SOPTWARE: MI
SEQ ID NO 25
LENGTH: 991
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: O'KEEPE, BRIAN
APPLICANT: O'KEEPE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
        Query Match 1.7%;
Best Local Similarity 51.2%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/09247373B Patent No. 6168954
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 106;
                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEPAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CLONE: SSM.PK0067.G5
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TISSUE TYPE: SOYBEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 991 base pairs
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NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: 1
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CLASSIFICATION: 435
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                                                                                                                                                                 Microsoft Office 97
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51.2%;
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ER: CL-1108
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        Score 45.4; DB 3;
Pred. No. 0.099;
0; Mismatches 101;
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                                       DB 3; Length 991;
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US-09-296-715-25
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                                                                Matches
                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: MCGONIGLE
APPLICANT: O'KEEFE,
                                                                                                                                                                                                                                                                                                                                          TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/296.715
FILING DATE:
                                                                                                                                           ORIGINAL SOURCE:
TISSUE TYPE: SOYBEAN
IMMEDIATE SOURCE:
CLONE: SSM.PK0067.G5
                                                                                                                                                                                                           MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
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ADDRESSEE: B.I. DU PONT DE
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                            2473 AAAAACATTGTTTCAGGAGAAGGGAGCATAAGTTTACAGCCTACAGGACGTACACAATAT 2532
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                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                         302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                            linear
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51.2%;
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ENZYMES
                                                              0,
                                                                             Score 45.4; DB 3; Pred. No. 0.099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEMOURS AND COMPANY
                                                                Mismatches
                                                                101;
                                                                                            Length 991;
                                                                Indels
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RESULT 8
US-09-103-840A-1
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US-09-103-840A-2
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                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.7%;
Best Local Similarity 52.1%;
       APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                        Sequence 1, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DIA SEQUENCES FOR STRATITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2436-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
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OTHER INFORMATION: "n" bases at various
OTHER INFORMATION: represent a, t, c or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Pred. No. 10;
0; Mismatches
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                              FOR STRAIN ANALYSIS IN MYCOBACTERIUM
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FILE REFERENCE: P3330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
PPIOT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
PPIOT APPLICATION TEMOVED - See Palm or File
NUMBER OF SEQ ID NOS: 550
LENGTH: 783
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                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-002-321
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                                                Query Match
Best Local Similarity
Matches 86; Conserv
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CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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APPLICANT:
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2522 GTACACAATATCCTGCTGCTGGGAAAACCACAGCATTTTATCTATTTTTATTTTAATAG 2581
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K
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                                                                Score 42.8; DB Pred. No. 0.41;
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Pred. No. 10;
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US-08-910-925-2/c
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Best Local Similarity 58.1
Matches 75; Conservative
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Patent No. 6162601
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatibl
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for W
                                                                                                                                                                                                                                                                                TOPOLOGY: lines
IMMEDIATE SOURCE:
LIBRARY: FIBRNO
CLONE: 53219
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REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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CORRESPONDENCE ADDRESS:
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APPLICANT: Shah, Purvi
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                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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1759 TCAGACATC 1767
                                                                                                                        1873 TGCTGCCACCTGTACTGGAGCTGCTACTGGAACTACTGCGACTGCTACTACTTCCACTGC
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                                                    TGGAACTACTTCCACTGCTACTGGTTGAACTGCTACTAGAACTGCTACTGCTACTGC 1754
                                                                                     TGTGAGCTCAACCTGGGTGACAAGTGTCTGGACGGCGTGCTGAACAACAACAGCTACGAG 1758
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Pred. No. 0.83;
0; Mismatches 54; Indels 0
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US-09-252-991A-2607
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                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2607
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PRIOR FILING DATE: 1998-C
NUMBER OF SEQ ID NOS: 331
SEQ ID NO 2607
LENGTH: 1734
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SEQ ID NO 2236
LENGTH: 966
TYPE: DNA
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                                                                                                                 Query Match
Best Local Similarity 54.9
Matches 85; Conservative
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TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS
TITLE REFERENCE: 107196.136
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
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Local Similarity 54.5%;
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134 CCTGGGGACGGCTCCTGCGTCTGGGCGCGGAGGGGGGGGCGAGCCGCACGTCCTCCTGAGGA 193
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                                                                   CGGGGATGTGAATCCCGATGGAGCGGCCCGAGGAAGGCAAGCAGTCGCCGCCGCCGCCGCAGC 133
                                       CGCTGCTGTTCATCGCCATCGATCGCCTGCAGCAACGCAAGGAGCAGCGCCTGGCGGAGG 1271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                  UMBER: US 60/094,190
1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rubenfield et al.
NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                     1.6%;
                                                                                                                   0
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                                                                                                                   Score 42.4; DB Pred. No. 0.79; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42.4; DB Pred. No. 0.58;
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                                                                                                                                                        DB 4;
                                                                                                               71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND THERAPEUTICS
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TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.10.2
CURRENT APPLICATION UNMEER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCTEP01/03971
PRIOR TILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-10-204-708-62/c
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US-09-252-991A-2445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-18
PRIOR APPLICATION UMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2445
LENGTH: 2016
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 62
LENGTH: 6801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62, Application US/10204708
5. 6677731
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Pred. No. 0.86;
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; ORGANISM: Buchnera
US-09-790-988-1
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APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SY
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
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US-09-790-988-1
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-62
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Patent No. 663293
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.6%;
Local Similarity 58.9%;
es 73; Conservative
                                                                                                                                                                                         625138 AAGGCTATCTATTATACAAATTTATATTTAAAAAGTAATTAACAATGGCCTCTTCAT
                                                                                            2584 TTGGTGCTTATCTTCTAATAAGATTTAAATGTCACAAACTGTAGCACAAATAATATAATT 2643
                                                                                                                                                        2464: AAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAGTTTACAGCCTACAGGACGT
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                                                                                                                                                                                                                                                        103;
                                                                                                                                                                                                                                                                                                                                                                  640681
                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Ver. 2.1
ACAAAATAAAAATAATAGAATAA
                             TATAATTTACAAATTGACAAAAA 2667
                                                                                                                              GCAAAATATTATGCAATTGGAAAAAGCACTGCTCTTTTTCTTTTTAATTATTATAAAAAA 625257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09790988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAA 2874
                                                               AAATTATTTTTCCTAAAAAAAAAGAAAACAGTGAGAATTTATTGAAAATAATCAATAAAG
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Pred. No. 19;
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 625341
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Search completed: January 15, Job time: 234 secs

2005, 06:21:34

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

20: /cgn2_6/ptodata/2/pubpna/US10B_PUB.seq:*

20: /cgn2_6/ptodata/2/pubpna/US10B_PUB.seq:*

20: /cgn2_6/ptodata/2/pubpna/US10B_PUB.seq:*

20: /cgn2_6/ptodata/2/pubpna/US10B_PUB.seq:*
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Gapop 10.0 , Gapext 1.0
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11090.227 Million cell updates/sec
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2679
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match Length DB ID	Length	DB	ID	Description
ا ا ا	1995	74.5	1995	و و	US-09-780-525-1	Sequence 1, Appli
N	1919.4	71.6	2448	16	US-10-108-260A-2073	Sequence 2073, Ap
ω	945	35.3	1311	ω	US-09-764-864-22	Sequence 22, Appl
4	876.2	32.7	2186	15	US-10-094-749-160	Sequence 160, App
_U	536.6	20.0	693	9	US-09-764-864-483	Sequence 483, App
6	394.4	14.7	476	10	US-09-918-995-2180	Sequence 2180, Ap
7	310.2	11.6	357	9	US-09-764-864-322	Sequence 322, App
8	273.6	10.2	449	10	US-09-918-995-13662	Sequence 13662, A
9	256.4	9.6	354	9	US-09-764-864-323	Sequence 323, App
10	256.4	9.6	354	ø	US-09-764-864-742	Sequence 742, App
11	60	2.2	60	10	US-09-908-975-6220	Sequence 6220, Ap
12	54.2	2.0	520	17	US-10-021-323-7699	Sequence 7699, Ap

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46.8	47	47.2	47.2	47.2	47.8	47.8	47.8	47.8	47.8	47.8		47.8	47.8	47.8	47.8	47.8	47.8	47.8	47.8	٠	48.8	49	49.4	49.4	49.4	49.4	49.4	50.2	51	51	51	
1.7	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8		1.8	1.8			1.8	1.8		1.8		1.8		1.8			1.8		1.8		1.9			1
487	349	6215	537	424	565	556	556	556	556	529	526	526	516	486	474	469	319	312	309	7455	373	434	554	537	486	469	433	526	995	411	383	1100
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US-10-021-323-2841	US-09-814-353-18039	US-10-311-455-1163	US-10-021-323-8120	US-09-960-352-11218	US-10-021-323-11125	US-10-357-930-43620	US-10-357-930-42124	US-10-357-930-40182	US-10-357-930-40082	US-10-021-323-10810	US-10-021-323-14764	US-10-021-323-14764	US-10-021-323-6457	US-10-021-323-6536	US-10-357-930-56511	US-10-021-323-16830	US-10-021-323-7947	US-09-960-352-8414	US-10-357-930-45013	US-10-311-455-1732	US-10-021-323-5700	US-09-960-352-3525	US-10-021-323-6039	US-10-021-323-1736	US-10-021-323-6536	US-10-021-323-16830	US-10-021-323-6681	-10	US-10-425-115-44403	US-10-424-599-127666	US-09-814-353-18006	
Sequence 2841, Ap		1163,	e 8120,		Sequence 11125, A	Sequence 43620, A	42124,	40182,	Sequence 40082, A	Sequence 10810, A	14764	14764		6536,		Ó	_	Sequence 8414, Ap	4501	Sequence 1732, Ap	0	3525,	6039,	1736,	Sequence 6536, Ap		6681,		Sequence 44403, A		Sequence 18006, A	,000,

ALIGNMENTS

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APPLICANT: Vuan Zhou
APPLICANT: Yuan Zho
APPLICANT: Yuan Zho
APPLICANT: Priya Chaturvedi
APPLICANT: Mark R. Hurle
APPLICANT: Mark R. Hurle
APPLICANT: Xiaotong Li
TITLE OF INVENTION: FHARI, A NEW RING FINGER PROTEIN
FILE REFERENCE: GP-70668-C1
CURRENT APPLICATION NUMBER: US/09/780,525
CURRENT APPLICATION NUMBER: US/09/780,525
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 09/456,876
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1995
TYPE: DNA
CORGANISM: HOMO SAPIENS
US-09-780-525-1
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                                                                                                                                                                      Query Match 74.5%; Score 1995; Dest Local Similarity 100.0%; Pred. No. 0; Matches 1995; Conservative 0; Mismatches
        151 CGTCTGGGCGGGAGGAGGGCGAGCCGCACGTCCTCCTGAGGAAGCGGGAGTGGACCATC 210
                                                                                              91 ATGGAGCGGCCCGAGGAAGCAAGCAGTCGCCGCCGCCGCAGCCCTGGGGAACGGCTCCTG 150
                                                                  1 ATGGAGCCGCCGAGGAAGGCAAGCAGTCGCCGCCGCCGCCAGCCCTGGGGACGGCTCCTG 60
                                                                                                                                                                                                                                   DB 9; Length 1995;
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Gaps

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8 B 8

SEQ ID N LENGTH TYPE: ORGANI	1231 GCCAGGAATAAAATCACTCAAGACATGCTGCAGCCCAAAGTCAGGCGGTCTTTTTCTGAT 1290	
CURRENT CURRENT NUMBER	1171 GCATACCTCATCCAGCATCCAGACAAGAGTGCGCAGTGAAGAAGATGTGCAAAGTATGGAT 1230	
GENERAL GENERAL APPLICA TITLE 0	1111 ACCTGCCGCTGTCCCGTGGAGCGGATCTGTAAAAACCACATCCTCAACAACCTCGTGGAA 1170	
RESULT 2 US-10-108- ; Sequence	1051 ATGCACACGITCTGCGGGGCTTGCTACTCGGGCTGGATGGAGGGCTCGTCCCTGTGTCCT 1110	
Db 1	991 ACGCTGACATGCATCTGCCAGGACCTGCTGCACTGCGTGAGTTTTGCAGCCCTGC 1050	
	931 GCCCAAACCGTCCACGAGGACGTCAGAGCAGCGGCTGGGAAGCCAGACAAGATGGAGGAG 990	
) B 4	871 AGAGGAGATGGGGACCTTGACCTGAACGGCAGTTGTTGGTCGCACAACCGCGTAGAAAT 930	
- L L	811 TCCTTTTCGTCGTTGGAACCCCAGGATCAGGAGGAGTTTGGAGCCCGTGAAGAAGAAAATG 870	
	751 TCTGTGGCAAGTGATGAAGTCTCCCAGCTTTGCCTCAGCTCTCCCAGACAGA	
	691 GAGCGTTCCTCCAGTTGTGGGTCTGGGGGTGGTGGCATCTCCCCTAAAGGAAGTGGTCCC 750	
0 0 4	631 ACGTCAGACCTCTTCCCCACAGGCCTCTTCCACGGAGCCTTCTCCTGCAGGGCGA 690	
	571 GTCCCTCCGTCGCCCGCCACTCAGGTGTGCTTTGAGGAACCACAGCCATCAACATCG 630	
OV 1	511 GTGTTCCATGGGACCAAAGATACCTCAGGTGCAGGTGCAGGGCGAGGGGCCGATCCCCGG 570	
Q	451 GAATCTTTAAGTGAAAAGCAAGGCATGACACAAGAATCCTTTGAAGCTAACAAGGAAAAT 510	
рь 1 Оv 1	391 GATGTCATCTACTTGGTGTACAGGAAGAATGAACCGGAACACAACGTGGCATACCTCTAT 450	
рь Оу 1		
Qγ 1	nati giragi isbatisaaraan caggi caggi gacactiggaa Agiigattaacaagci saaggii gitaagaagcagacatigo	
Db 1	71 TGTAGAATTGTAGTGGATGAAAAATCAGGTCAGGTGACACTGGAAGATACCAGCACCAGT 33	
Db 1	211 GGGCGGAGACGATGCGACCTTTCCTCCCAGCAATAAACTGGTCTCTGGAGATCAC 180	
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WS-10-108-260A-2073
; Sequence 2073, Application US/10108260A
; Dublication No. US20040005560A1
; GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
ITILE OF INVENTION: NO. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PATENTIN VEY. 2.1
; SEQ ID NO 2073
; LENGTH: 2448
; TYPE: DNA
; ORGANISM: Homo sapiens

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78 TCATCCAGCATCCAGACAAGAGTCGCAGTGAAGAAGATGTGCAAAGTATGGATGCCAGGA 12 	≨—≨ —6 —6	1058 CGTTCTGCGCGCGCTTGCTACTCGGGCTGGATGGAAGCGCTCGTCCTGTGTCCTACCTGCC 1117	998 CATGCATCATCTGCCAGGACCTGCAGGACTGCGTGAGTTTGCAGCCCTGCATGCA	38 CCGTCCACGAGGACGTCAC	878 ATGGGGACCTTGACCTGAACGGGCAGTTGTTGGTCGCACAACCGCGTAGAAATGCCCAAA 937 	818 CGTCGTTGGAACCCCAGGATCAGGAGGAGTTTGGAGCCCCGTGAAGAAAATGAGAGAAG 877	758 CAAGTGATGAAGTCTCCAGCTTTGCCTCAGCTCTCCCAGACAGA	698 CCTCCAGTTGTGGGGTCTGGGGGTGGTGGCATCTCCCCTAAAGGAAGTGGTCCCTCTGTGG 757	63B ACCTCTTCCCCACAGCCTCGGCCTCTTCCACGGAGCCTTCTCCTGCAGGGCGAGAGAGGCGTT 697 357 356	57	78 CGTCGTCGCCCGCCACTCAGGTGTGCTTTGAGGAACCACAGCCATCAACATCGACGTCAG 63	518 ATGGGACCAAAGATACCTCAGGTGCAGGTGCAGGGCGAGGGGGCCGATCCCCGGGTCCCTC 577	458 TAAGTGAAAAGCAAGGCATGACACAAGAATCCTTTGAAGCTAACAAGGAAAATGTGTTCC 517	398 TCTACTTGGTGTACAGGAAGAATGAACCGGAACACGTGGCATACCTCTATGAATCTT 457	338 TGATTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCTTTACAGACTGGGGATGTCA 397	278 TTGTAGTGGATGAAAATCAGGTCAGGTGACACTGGAAGATACCAGCACCAGTGGAACAG 337 	218 GACGAGGTTGCGACCTTTCCTCCCCAGCAATAAACTGGTCTCTGGAGATCACTGTAGAA 277	y Match 71.6%; Score 1919.4; DB 16; Length 2448; Local Similarity 88.5%; Pred. No. 0; hes 2227; Conservative 0; Mismatches 6; Indels 284; Gaps 2;	8-260A-2073
D Qy	B 8	gb 45	S B	Q B	8 8 8	S & &) B &	5 B 2	S B	Q 8	g &	B &	? B #	S B 2	? B !	S B &	;	\$ \$	§
2190 AGGGACGCAGGGTCTCCGACAGGTGCTCTGGGGTGACTCTTCTGTGGAGCTTTTTACCCT 2249	2130 AGCGTGTTTTTAAATRCAGAGACAAGGACGTGTCAAGGTGTTTTCACAGCCCCCTGAGGGA 2189	787	.727 CTGCCGCACTCAGGTGAAAGCTCACCACGCCATGAAATTCAATCATCATCTGAACAGAC		TCCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTGACTGCTAACTGGGGGCCGTAA	1890 GENERAL CENTRAL CONTROL C	GAGGATTACC SCINCCAGASCII SACAI SAMANAA I SACCAGAGACCICGI IIIIIIIIIIIIIIIIIIIIIIIII	1770 GAAGAATTTAGGGGAAGGGGGGGGGGGGGAAGAACAACAAGGGAAGAGGGGGG	GCTTTCCTGCGACATCATTATAAACAGGTAACATTTGCCCCTTCATCTCGGCAGAGCTCAA	1702GAGCTCAN 1709	GCTGCACCCGGACCGGCTGCCTACGGCTGCCCGGTTTTGT	1396 GCGTGTGCCCCTCAGCAGTGTGCGGTCTGCCGCCTCTGCAGCCTTTCTGCCACCTGTACTGGG 1306		1538 CCCTTGTGCTTGCTTCCAACCCCAAGGACTCGAAGGAGCGGAGCGAGC		1418 ACTGCCCAGCACCCGAGGGCCGAGGCCCCCCCAGGGCCCCCCC			1238 ATAAAATCACTCAAGACATGCTGCAGCCCAAAGTCAGGCGGTCTTTTTCTGATGAAGAAG 1297

Oy 56 TCCGGGTTCGCCGCGGGGCGGGGATGGAATCCCGATGGAGGCCCCGAGGGAGG	PEATURE: NAME/KEY: SITE LOCATION: (1281) OTHER INFORMATION: n equals a,t,g, or c -09-764-864-22 -09-764-864-22 Query Match Best Local Similarity 81.1%; Pred. No. 1.7e-243; Best Local Similarity 81.1%; Pred. No. 1.7e-243; Matches 1267; Conservative 6; Mismatches 7; Indels 282; Gaps	Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 22 LENGTH: 1311 TYPE: DNA ORGANISM: Homo sapiens	US-09-764-864-22 ; Sequence 22, Application US/09764864 ; Patent No. US20020132753A1 ; GENERAL INFORMATION: ; APPLICANT: Rosen et al. ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies ; FILE REFERENCE: PTZ23 ; CURRENT APPLICATION NUMBER: US/09/764,864		Db 2147 TCTGTTTTCAGGAAAAGTTTCAAGGGGAAGGGCAAGTTTATCAAAAAACATTGTTTCAGG 2206 Qy 2490 AGAAGGGAAGATTTACAGCCTACAGGGAGGGCAAGATTATCCTGCTGCTGCTGGAAAAC 2549 Db 2207 AGAAGGGAGCATAAGTTTACAGCCTACAGGACGTACACAATATCCTGCTGCTGCTGGAAAAC 2566 Qy 2550 CACAGCATTTTATCTATTTTTATTTTAATAGGTTTTGGTGCTTTTTTATCTTCTTAATAAGATTT 2609	Qy 2250 CTGAGTGAGACCCTCCCCAGAGCCCCGGGGGCCGCCCTCCTGGTGAGCGCTGG 2309
Db 809 TISTANAAACCACATCCTCAAACAACTCTCGTGGAAGCATACCATCATCCAGCACCACACCACCACACCACCAGGAATAAAATCAACCACACCAGGAATAAAATCAACCACACCAGGAATAAAATCAACCACACCAGGAATGAAAATAAAATCAACTAAGACA	Oy 1016 ACCTGCTGCACGACTGCGTGAGTTTGCAGCCCTGCATGCA	Qy 896 ACGGGCAGTTGTTGGTCGCACAACCGCGTAGAAATGCCCAAAACCGTCCACGAGGACGTCA	OY 776 GCTTTGCCTCAGCTCTCCCAGACAGAAAGACTGCGTCCTTTTCGTCGTTGGAACCCCAGG	Oy 656 CGGCCTCTTCCACGAGCCTTCTCCTGCAGGGCGAGAGCGTTCCTCCAGTTGTGGGTCTG		

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PRIOR APPLICATION NUMBER: JF 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 160
LENGTH: 2186
TYPE: DNA
ORGANISM: Homo sapiens
US-10-094-749-160
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US-10-094-749-160
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Best Local Similarity
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                                                                                                                                                                                        Matches 890;
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APPLICANT:
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TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
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                           GITACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGCAGAACATTC 1951
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                                                                                              CTCTCCAGCGGGGAGTGTTTCTGCTGTCTGATTACAGAGTCACGGGAGACACCGTTCTGT
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OTSUKI, TETSUJI
WAKAMATSU, AI
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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IRIE, RYOTARO
TAMECHIKA, ICHIRO
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                                                                                                                                                                                     Score 876.2; DB 15;
Pred. No. 7.8e-225;
0; Mismatches 3;
                                                                                                                                                                                                                     Length 2186;
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US-09-764-864-483
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                                                                                                                                                                                                Sequence 483, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                        Prior application data removed -
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 483
LENGTH: 693
TYPE: DNA
ORGANISM: Homo sapid
FEATURE:
NAME/KEY: SITE
LOCATION: (11)
OTHER INFORMATION: r
NAME/KEY: SITE
LOCATION: (13)
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; Sequence 2180, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
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Best Local Similarity
Matches 608; Conserv
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-09-764-864-483
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OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (670)
OTHER INFORMATION: n e
NAME/KEY: SITE
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OTHER INFORMATION: I
NAME/KEY: SITE
LOCATION: (690)
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LOCATION: (623)
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NAME/KEY: SITE
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FITTLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTITIES OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCES: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2180
WS-09-764-864-322
US-09-764-864-322
; Sequence 322, Application US/09764864
; Patent No. US20020132753A1
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Best Local Similarity
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NAME/KEY: misc_feature
LOCATION: (1)...(476)
OTHER INFORMATION: n =
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ORGANISM: Homo sapiens
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                                                                                                                                                                              CCGAAACTACAGTTAAAGCGGAAGTCTGTTTTCATGAATAGTTTCAAGGGAGAAGGGCTA 469
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Pred. No. 2.2e-95;
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; Prior application data removed - co NUMBER OF SEQ ID NOS: 1792 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 322 LENGTH: 357 ; TYPE: DNA ; ORGANISM: Homo sapiens

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23

and

Antibodies

CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17

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file wrapper

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APPLICANT: Hyseq, Inc.
ITITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
ITITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
FRIOR APPLICATION NUMBER: US/09/235,076
FRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13662
LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; NAME/KEY: SITE
; LOCATION: (272)
; OTHER INFORMATION: n equals a,t,g, or
; NAME/KEY: SITE
; LOCATION: (300)
; OTHER INFORMATION: n equals a,t,g, or
US-09-764-864-322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ঠ
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US-09-918-995-13662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13662, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                           Query Match 10.2%;
Best Local Similarity 98.6%;
Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 345; Conserv
                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(449)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                  2447
                                                                                2387
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                                                TTG-TTAAGAAGCAGACATGCCC-TTTACAGACT-GGGGATGTCATCTACTTG 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCGGGTTCGGCGCGGGGGGGGGATGTGAATCCCCGATGGAGCGGCCCGAGGAAGGCAAGC
TTTCAAGGGAGAAGGGCAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGTTTÄÄGAÄACÄGÄCÄTGCCCTTTTÄCÄGÄCTGGGGGATGTCATCTACTTG
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ilarity 97.7%;
Conservative
                                                                                                            Score 273.6; DB 10;
Pred. No. 7.4e-63;
0; Mismatches 4;
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Pred. No. 8.9e-73;
0; Mismatches 5;
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                                                                                                                                            DB 10; Length 449;
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                  2506
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S S B	94 TITCAAGGGAGAAGGGCAAGTITATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAGTT 153 2507 TACAGCCTACAGGACGTACACAATATCCTGCTGCTGGGAAAACCACAGCATTTTATCTAT 2566
טט	INCHRECTIACHARAHAMIATELIRETRETRETRETRETRETRETRETRETRETRETRETRETR
, &	2567 TTTTTATTTTAATAGGTTTTGGTGCTTATCTTCTAATAAGATTTTAAATGTCACAAACTGTA. 2626
Db	214 TTTTATTTTAATAGGTTTTGGTGCTTATCTTCTAATAAGATTTAAATGTCACAAACTGTA 273
Ş	2627 GCACAAATAATAATTTATAATTTACAAATTGACAAAAA 2666
Db	274 GCACAAATAAATTTATAAATTTACAAATTGACTAAAA 313
RESULT 9 US-09-764 ; Sequent	RESULT 9 US-09-764-864-323 , Sequence 323, Application US/09764864
; GENERAI	
; FILE REF	APPLICATION: NUCLEIC ACIUS, FIOCEILS, GIO AIG BRINGE: PTZ23 APPLICATION NUMBER: US/09/764,864
CURRE!	FILING DATE: plication dat
	SEQ ID NOS: 1792 PatentIn Ver. 2.0
	354 NA
	NAME/KEY: SITE
	INFO
; LOCA: ; OTHEI US-09-76	LOCATION: (313) OTHER INFORMATION: n equals a,t,g, or c 9-764-864-323
Query Match Best Local Matches 26	<pre>Match 9.6%; Score 256.4; DB 9; Length 354; DCal Similarity 93.3%; Pred. No. 2.8e-58; DCal Similarity 93.3%; P</pre>
γŞ	221 GAGGTTGCGACCTTTCCCTCCCAGCAATAAACTGGTCTCTGGAGAGATCACTGTAGAATTG 280
Ъ	27 GAGATAAGGGACCTGACTTCCCCWGCAATAAACTGGTCTCTGGAGATCACTGTAGAATTG 86
Ş	281 TAGTGGATGAAAAATCAGGTCAGGTGACACTGGAAGATACCAGCACCAGTGGAACAGTGA 340
Db	87 TAGTGGATGAAAATCAGGTCAGGTGACACTGGAAGATACCAGCACCAGTGGAACAGTGA 146
δ	341 TTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCTTTACAGACTGGGGATGTCATCT 400
DЬ	147 TTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCTTTACAGACTGGGGATGTCATCT 206
8	401 ACTTGGTGTACAGGAAGAATGAACCGGAACACAACGTGGCATACCTCTATGAATCTTTAA 460
В	207 ACTTGGTGTACAGGAAGAATGAACCGGGAACACGTGGCATACCTCTATGAATCTTTAA 266
Ş	461 GTGAAAAGCAAGGCATGACACAAGAATCCTTTGAAGCTAACAAGG 505
Вb	267 GTGAAAAGCAAGCATGACACANGAATCCTTTTGATACCTCAGGG 311
RESULT 10 US-09-764-	0 4-864-742

; Sequence 742, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

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APPLICANT: WASSERMAN, AVI
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Liat
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: Patentin version 3.0
TRUCTH: 60
                                                         ; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo s
US-09-908-975-6220
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; OTHER INFORMATION: n equals a,t,g,
; NAME/KEY: SITE
; LOCATION: (313)
; OTHER INFORMATION: n equals a,t,g,
US-09-764-864-742
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local
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CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 354
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAGTGGATGAAAAATCAGGTCAGGTGACACTGGAAGATACCAGCACCAGTGGAACAGTGA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGATAAGGGACCTGACTTCCCCCWGCAATAAACTGGTCTCTGGAGATCACTGTAGAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGTGGATGAAAAATCAGGTCAGGTGACACTGGAAGATACCAGCACCAGTGGAACAGTGA
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                                                                           sapiens
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2.2%;
Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.8e-58;
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DB 10;
8.6e-06;
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                Length
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APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 95539
LENGTH: 1255
TYPE: nw.
                                                                                                                                                                                                                                                                                        RESULT 13
US-10-424-599-95539
; Sequence 95539, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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US-10-021-323-7699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Deikman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 7699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Gossypium hirsutum
LOCATION: (1)..(1255)
OTHER INFORMATION: unsure at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: LIB3828-019-Q1-N6-D6
                                                 FEATURE:
                                                                ORGANISM: Glycine
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                              NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 АЛЛАЛАТТТАЛАЛАЛАЛАЛАЛАЛАЛАССТАЛАЛАТТТТАЛАЛАЛАДАЛАЛАЛАЛАЛАЛАЛА 258
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; ORGANISM: Homo sapiens
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US-09-814-353-18006
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RESULT 15
US-10-424-599-127666/c
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SOFTWARE: FastSEQ for
SEQ ID NO 18006
LENGTH: 383
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Best Local Similarity
Matches 78; Conserv
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APPLICANT: Thompson, Pamela
APPLICANT: Lillle, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METH
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/216,820 FILING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/257,672 FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/220,661 FILING DATE: 2000-07-25
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                                                                         AAA 238
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Pred. No. 0.0064;
0; Mismatches 4
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Pred. No. 0.0097;
0; Mismatches 71; Indels 0;
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Job time : 1397 secs
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_86287C.1
US-10-424-599-127666
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APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28
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SEQ ID NO 127666
LENGTH: 411
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                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
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                                                                                                                  2677 AAA 2679
                                                                                                                                                                                           2557 TTTTATCTATTTTTATTTTAATAGGTTTGGTGCTTATCTTCTAATAAGATTTAAATGTC 2616
                                                                                                                                                        156 ААААЙТТТТАААЙААЙААЙТААЙААААТАКТАССТАЙАЙААЛАЙАЙАЙЙААЛАЙЙАААА
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Pred. No. 0.0066;
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Perfect score:
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AK027687 Homo sapi

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AX405642 Sequence

AX877222 Sequence

BD156548 Primer fo

AK01658 Homo sapi

AX834949 Sequence

AK097671 Homo sapi

BD183291 Novel gen

AK090948 Homo sapi

AX713476 Sequence

AK054917 Homo sapi

CQ71982 Sequence

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/ ob_artem= none septems /mol_type="unassigned DNA" /db_aref="taxon:9606"	Research	Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: RP 1074617-A 12099 07-RB-2001:	Homo sapiens 'Indinali', Homo sapiens 'Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AX877194.1 GI:40031930		091 A111A1A911 KAAMA1 KACAMAMAMAMAMAMAMA 2079 	501 YOUTH THE THE THE THE THE THE THE THE THE T	521 CGTRUCACARIA ICCIGCIGGIGADARACUACAGURIIIIACIA IIIIAANA	GCCAAGIIIA CAMPAGAIIGIII CAMBAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	######################################		CCGCAGCCCCCCCCCCTGGTGAGCGCCTGGGCAGAGAGGCCAGTCTGTGCTACCAGCAGAGA	GETEACL LIE IE IEGNECITIATE LIE IEGNECITIATE LIE IEGNECITICATE AGNECITATION DE CONTROL D	CAMAGISTITICACAGCCCCCTGAGGGAAGGGACGCAGGGTCTCCGACAGGTGCTCTGG TCAAGGTGTTTTCACAGCCCCCTGAGGGAAGGGA	GRICHAGETTICAGCACTIGAGGGIAAGGAGAGCGIGTITTTAAAATTACAGAGACAAGCGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGI	A CONCERNICA CON CINCAN CONCENTRATION AND A CONCENTRATION AND ACCORDING CONCENTRATION OF A CONCENTRATION OF	TCCCGTCCTGACTGCTACTGGGGCCGTAACTGCCGCACTCAGGTGAAAGCTCACCACGCCCCCCCC	921 GAGCTGACCTATCAGTATCGGCAGAACATTCCTGCTTCCGAGTTGCCAGTGGCCGTAACA 1980

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GCDLSPFSNKLVSGDHGRIVDEKSGQVTLEDTSTSGTVLNKLKVVKKQTCPLQTGDV
IYLVYRKNEPEHNVAYLYESLSEKQGMTQSFDTSTSGTVLNKLKVVKKQTCPLQTGDV
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RAAGKPDKMEETLTCI CQDLLHDCVSLQPCMHTFCAACYSGMMERSSLCPTCRCPV
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CTCAGGTGTG	GCAGGTGC	79.6%; ; 100.0%;	/organism="Homo sapiens /mol_type="genomic DNA" /db_xref="taxon:9606"	Location/Qualifie (79) Location/Qualifiers	.5/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/ Ber for synthesizing full-length cDNA and use thereof FH	SAITO, JUNICHI YAMAMOTO, S KEIICHI NAGAI, TETS	191363-A/1 2002 2000 JP 20	r for synthesizing f t: JP 2002191363-A 1 RESEARCH INSTITUTE Homo sapiens (human)	to 2639	63-A/113 8 (human	34 for synthesizing 34 34.1 GI:27862292		acaaataataattitataattitacaaattgac 	TATTTTAATAGGTTTGGTGCTTATCTTCTAATAAGATTTAAATGTCACAAACTGTAG 	CAGCCTACAGGACGTACACAATATCCTGCTGCTGGGAAAACCACAGCATTTTATCTATTT	CAAGGGAGAAGGGCAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAGTTTA 	GCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAAGTT
CTTTGAGGAACCACAGCCATCAACATCGACGT CTTTGAGGAACCACAGCCATCAACATCGACGT	GGTGCAGGGCGAGGGGCCGATC	core 2133; DB 6 Pred. No. 0; Mismatches	no sapiens" nomic DNA" nn:9606"	lalifiers (79) . (2034). Lifiers	7K16/18,C12N1/15, 3//C12P21/08,G06F		7 80990 GAI TETSIO	full-length cDN 11377 09-JUL-20 'E	Primates; Catarrhin) Nishikawa,T., Hayash	1 2 5 7 8 7 8	2639 bp DNA linear full-length cDNA and use		TTACAAATTGAC 2661	Taataggtttggtgcttatcttctaataagatttaaatgtcacaaactgtag 	TATCCTGCTGCTGGGA	ATCAAAAACATTGTTT ATCAAAAACATTGTTT	AACTACAGTTAAAGCA
CATCGACGTCAGACCT	CCCGGGTCCCTCCGTC	; Length 2639; 0; Indels 0;			C12N1/19,C12N1/2: 17/30,C12N15/00,(NA and use there	TOMOYASU SUGIYAMA,AI	NISHIKAWA KOJI HAYASHI KAORII	A and use thereo	inidae, Saito,F	Vertebrata. Ruti	linear PAT A and use thereof		4 0	atttaaatgtcacaaa atttaaatgtcacaaa	CTGCTGCTGGGAAAACCACAGCATTTTATCTATTT 	Caggagaaggagcati Caggagaagggagcati	GAAGTCTGTTTTCAGG
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CDS	FEATURES source			RS PL	TITLE	JOURNAL PUBMED REFERENCE AITTHORS	TITLE						•	AUTHORS	ORGANISM
<pre>/cell_line="NT2" /cell_type="teratocarcinoma" /clone_libe"NT2RP4" /note="cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction." 792037 /note="unnamed protein product" /codon start=1 /protein_id="BAB55297.1"</pre>	University of Tokyo. Location/Qualifiers 12639 /organism="Homo sapiens" /mol_type="mRNA" /mol_type="mRNA" /db_xref="taxon:9606" /clone="NT2RP4000455"	Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,	Submitted (10-MAY-2001) Takao Isogai, Helix Re Submitted (10-MAY-2001) Takao Isogai, Helix Re Genomics Laboratory; 1532-3 Yana, Kisarazu, Cf (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975 NEDO human cDNA sequencing project supported b	Unpublished 3 (bases 1 to 2639) 1 segai, T. and Otsuki, T. pirer Submission	Nishikawa, T., Nagai, K., Sugano, S., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Sasaki, N. NEDO human CDNA sequencing project	Nat. Genet. 36 (1), 40-45 (2004) 14702039 Teograf T Ota T Havashi K Siciyama T Ot	Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano Complete sequencing and characterization of 21,243 full-length human CNNac	Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Mat Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M. Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Na Satoh T. Shirai Y. Takahabi Y. Nakarawa K.	Kumagai, , Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Tashiro, H., Tirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Tirao, K., Tirao, K., Wawarami, T., Kobatake, N., Tirao, K., Tirao, K., Kawarami, K., Wawarami, Tirao, K., Kawarami, K., Ka	Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A. Goto,Y., Shinizu,F., Wakebe,H., Hishigaki,H., Sugiyama,A. Takemoto M. Kawakami B. Yamazak	Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi Fujil, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki N., Aortsuka S. Yoshikawa Y. Matsunawa H. Tohihara T.	Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Kat Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibas Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Hiracka S. Chiha Y. Tahida S. Ono Y. Takida	Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Is Nagahari,K., Murakami,K., Yasuda,T., Kwayanagi Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., K., Sugawara,M., Takhhashi,M., Kanda,K., Yokoi,T.	1 Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine M. Ohayashi,M. Nishi,T. Shihahara T. Tanaka T.,	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Qy 1129 GAGCGGATCTGTAAAACCACATCCTCAACCAACCTCGTGGAAGCATACCTCATCCAGCAT 1188	901 GACGTCAGAGCAGCGGCTGGGAAGCCAGACAAGATGGAGACGCTGACATGCATCATC 1009 TGCCAGGACCTGCTGCACACGACTGCGAGACTTTCTGCGCG 1	Qy 829 CCCCAGGATCAGGAGGATTTGGAGCCCGTGAAGAAGAAAATGAGAGGAGATGGGGACCTT 888	709 GGGTCTGGGGGTGGCATCTCCCCTAAAGGAAGTGGTCCCTCTGTGGCAAGTGATGAA 76	OY 589 GCCACTCAGGTGTGCTTTGAGGAACCACAGCCATCAACATCGACGTCAGACCTCTTCCCC 648	Query Match 79.6%; Score 213; DB 9; Length 2639; Best Local Similarity 100.0%; Pred. No. 0; Matches 2133; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 529 GATACCTCAGGTGCAGGTGCAGGGGCGATCCCCGGGTCCTCCGTCGTCGCCC 588	/db_xref="GI:14042553" /translation="MERPEEGKQSPPPQPWGRLLRLGAEEGEPHYLLRKREWTIGRRR GCDLSFPSNKLVSGDHCRIVVDEKSGQVTLEDTSTSGTVINKLKVVKKQTCPLQTGDV IYLVYRKNEPEHHVAXLYESLSEKQGMTQSFDTSGAGAGAGADRRVPPSSSPATQVCF EEPQPSTSTSDLFPTASASSTEPSPAGRERSSSCGSGGGISFKGSGFSVASDEVSSF ASALPDRKTASFSSLEPQDQEDLEPVKKXKRGGDLDLLAQDFRNAQTVHEDV RAAAGKPDKMEETLTCIICQDLLHDCVSLQPCMHTFCAACYSGMMERSSLCPTCRCPV ERICKNHILNNLVZAYLIQHDKSRSEEDVQSMDARNKITQDMLQPEVRRSFSDEEGS SEDLLELSDDUSSSSDIQOPYVCTQPFXARAGAQPPHCPAPEGEAPQALGDAPS SSDLLELSDDUSSSSDIQOPYVCTQCPTRASREDDTRVAPQCCAVCLQPFCHL YMGCTRTGCYGCLAPFCELNLGDKCLDGVLNNNSYESDILKNYLATRGLTMKNMLTES LVALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASELPVAVTSRPDCY WGRNCRTQVKAHHAMKFNHICEQTRFKN" ORIGIN
2161 CAGGTGCTCTGGGGTGACTCTTCTGTGAGGCTTTTACCCTCTGAGGAGACCCCCCAT 2269 GAGCCCCGGGGGCCGCAGCCCCCCCTCTGGTGAGACGCTCTGGGGGGGCAGGCTCGTGGTGGCAT [Db 1981 GCTCACCACGCCATGAAATTCAATCATATCTGTGAACAGACAAGGTTCAAAAACTAAGCA 2040 Qy 2089 TCCAGAGGCCCTGAGCAGCTTTCAGCACTGGAGGTGAAGAGAGAG	2 1 1 1 1	OY 1789 AGAGGTTTGACATGGAAAAACATGTTGACCGAGGAGCCTCGTGGCTCCCAGCGGGGAGTG 1848	Oy 1689 ACCGGCTGCTACGGCTGCCGGTTTTGTGAGCTCAACCTGGATGACAAGTGTCTG 1728	1549 TROTTECTACCCCATECTCCAACCCCAAGACCCGAACCAGAACCCGCGTGTCCGCCGCGTGTCCGCCGCGTGTCCGCCGCGTGTCGCCCCACCCGAACCAGACCCGAACACCCCACCACCCGAACACCCCAACCCGAACCAGACCCGAACCAGACCCGAACCAGACCCGAACCAGACCCGAACCACC	GACCTGCTGGAGCTGTCAGACGTTGACAGTGAGTCCTCAGACATTAGCCAGCC

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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetcow, K.H., Schaefer, C.F., Bhat, N.K.,

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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and mouse cDNA sequences
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guetticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee,
                                                                                                                    cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Cor DNA Sequencing by: Genome Sequence Centre, BC Canner Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Homo sapiens checkpoint with forkhead and ring finger domains, mRNA
(CDNA clone MGC:19963 IMAGE:4650348), complete cds.
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Proc. Natl. Acad. Sci. U.S.A. 9
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8922674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found
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/protein id="AAH12072.1"
/db xref="GI:15082330"
/db xref="LocusID:55743"
/db xref="MIM:605299"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="HRD1; Region: COG5243, HRD1, HRD ubiquitin ligase complex, ER membrane component [Posttranslational
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SEDLLELSDVDSESSDISQPYVVCRQCPEYRRQAAQPPHCPAPEGEPGAPQALGDAPS
TSVSLTTAVQDYVCPLQGSHALCTCCFQPMPDRRVEREQDPRVAPQQCAVCLQPFCHL
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                                                                                                                                                                                                                                                                                                                                                                            modification, protein turnover, chaperones]"
/db_xref="CDD:COG5243"
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LVALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASELPVAVTSRPDCY
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/note="FHA; Region: FHA domain.
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/mal_type="mENA"
/mal_type="mENA"
/db_xref="taxon:9606"
/clone="MGC:19963 IMAGE:4650348"
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3181 bp DNA linear PAT 14-JUN-2002 ence 57 from Patent WO0222660. 5642. 5642.1 GI:21438723 sapiens (human) sapiens sapiens (homan)	≥—≥			SCAGCAGAGACGAAGCCTTTCTGTAACATGCGGCCGTCCCGCCGAGAGGGGCAGTTTT 2270 CTTTTGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAGTT 2448		CONCERGES TO ACCOUNT TO THE CONTROL OF THE CONTROL	ACAAGCACGTCAAGGTGTTTTCACAGCCCCCTGAGGGAAGGGACGCAGGGTCTCCGA 2208	AGAGGCCCTGAGCAGCTTTCAGCACTGGAGGTGAAGAGAGCGTGTTTTTAAAATACA 2148 	CACCACGCATGAAATTCAATCATATCTGTGAACAGACAAGGTTCAAAAACTAAGCA 2088 	GCCGTAACATCCCGTCCTGACTGCTACTGGGGCCGTAACTGCCGCACTCAGGTGAAA 2028 	AGCTTCCGTGAGCTGACCTATCAGTATCGGCAGAACATTCCTGCTTCCGAGTTGCCA 1968 	TTTCTGCTGTCTGATTACAGAGTCACGGGAGACACCGTTCTGTGTTACTGCTGTGGCCTG 1908 	AGSTITUSCATGAAAAACATGTTGACCGAGAGCCTCGTGGCTCTCCAGCGGGGAGTG 1848	

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1129 GAGCGGATCTGTAAAAACCACATCCTCAACAACCTCGTGGAAGCATACCTCATCCAGCAT 1188	1009 TGCCAGGACCTGCTGCACGACTGCGTGAGTTTTGCAGCCCTGCATGCA	GACCTCAGAGCAGCTGGTAGGAAGCCAGACAAGATGGAGAAGCGTGACATCATC 89 GACCTGAACGGGCAGTTGTTGGTCGCACAACCGCGTAGAAATGCCCAAAACCGTCCACGAG	*** FILECOAGGITTUCCICAGECTAGACAGAAAGACTGGGTCCTTTTCGTCGTTGGAA 828	60.4%; Score 1618; DB 6; Length 3181; milarity 99.7%; Pred. No. 0; Conservative 0; Mismatches 3; Indels 2; Gaps GGTCTGGGGGTGGCATCTCCCTCAAAGGAAGTGGTCCCTCTGTGGCAAGTGATGAA	L438724" L438724" MERPEGKC HCRIVVDE KXIYESISS GGSGFSVAS GMERSSLCE AMERSSLCE AMERSLCE AMER	/organism="nomo sapiens" /mol type="unassigned DNA" 961967 /note="taxon:9606"	Mammalia; Eutheria; Primates; Ca Tang,Y.T., Liu,C., Zhou,P., Asun Xue,A.J., Yang,Y., Wehrman,T. an Novel nucleic acids and polypept Patent: WO 0222660-A 57 21-MAR-2 HYSEQ, INC. (US) Location/Qualifiers 1. 3181
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69 GTCTCCAGCTTTGCCTCAGCTCTCCCAGACAGAAAGACTGCGTCGCTTTTCGTCGTTGGAA	y Match Local Similarity 99.6%; Pred. No. 0; Local Similarity 99.6%; Pred. No. 0; hes 1945; Conservative 0; Mismatches 6; Indels 2; Gaps 1; 709 GGGTCTGGGGTGGTGGTCCCCCTAAAGGTAGTGGTCCCTCTGTGGCAAGTGATGAA 768	/procen_io="CAR89826.1" //db_xref="01:40031959" //db_xref="01:40031959" /translation="MERPEEGKQSPPPQPWGRLLRLGABEGEPHVLLRKREWTIGRRR GCDLSFPSNKLVSGDHCRIVVDERSGQVTPSTSTSGTVLNKLKVVKKQTCPLQTGDV IYLVYRKNEPBEHVVALLYESLBEKQGMTQBSFENVPCCYAQAGLKLLGSSDPTLASQ SIVITGSGGGGISPKGSGPSVASDEVSSFASALPDRKTASFSSLEPQDQEDLEPEKKK MRGDGDLDLNGQLLVAQPRRNAGTVHEDVRAAAGKPDKWEETLTCIICQDLHDCVSL QPCMHTPCAACYSGMWERSSLCPTCCEVFERICKHILMNLVAPALIQHPDKSRSEED VGSMDARNKITQDMLQPKVRRSFSDEEGSSEDLLELSDVDSESSDISQPYVVCRQCPE YRQAAQPPHCPA.PEGEPGALGDAPTSVSLITTAVQDYVCPLQGSHALCTCCFQP MPDRRABERGDPBRVAPQGCAVCLOPFCHLYWGCTRTGCYCCLAPFCELNLDGKCLDGV LNNNSYESDILKNYLATRGLTWKNMLTESLVALQRGVFLLSDYRVTGDTVLCYCCGLR SFRELTYQYQQNIPASBELPVAVTSRPDCYWGRNCETQVKAHHAMKFNHICEQTRFKN"		S Ota,T., I Ishii,S., Primers f Patent: E Research rce		7 2 AX877222 2 AX877222 3138 bp DNA linear PAT 17-DEC-2003 20 AX877222	2629 ACAARTAATATAATTTATAATTTACAAATTGAC 2661 	2569 TTTATTTTAATAGGTTTGGTGCTTATCTTCTAATAAGATTTAAATGTCACAAACTGTAGC 2628 	2509 CAGCCTACAGGACGTACACAATATCCTGCTGCTGCGGAAAACCACAGGATTTTATCTATTT 2568	2449 TCAAGGGAGAAGGCCAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAGTTTA 2508 	2389 GCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAGTT 2448 2269 GCTCTTTGTACATTTTCCGAAACTACAGTTAAAGCGGAAGTCTGTTTTCAGGAAAAGTT 2328
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 3138)

S Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamot.

Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.

Primer for synthesizing full-length cDNA and use thereof

Primer i JP 2002191363-A 11391 09-JUL-2002;

HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)

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PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAWA, AI WAKAMATSU PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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ner for synthesizing full-length cDNA and use thereof FH F
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KEIICHI NAGAI,TETSUJI OTSUKI
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/db_xref="taxon:9606"
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Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 15:22-3 Yana, Kisarazu, Chiba 292-0812, Japan (Bemall:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan, CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center
                                                                                                                                                                                                                                                                                                 3 (bases 1 to 3138)
Isogai, T. and Otsuki, T.
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Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakam
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Kimura, K., Makita, H.,
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                                                   CCAGACAAGAGTCGCAGTGAAGAAGATGTGCAAAGTATGGATGCCAGGAATAAAATCACT
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gcolispesnklyggdhcrivuslskgovytledystegytiniklkvykkotceljotgdv

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voshdarnkitomhlopkvrrssboledgssedllelsdvdsessdisopvvcroccpe

vrardadpphcpapegebcapollgdretssblielsdvsessdisopvvcroccpe

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/db_xref="taxon:9606"
/clone="NT2RP4000648"
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/proteIn_id="BAA91817.1"
/db_xref="GI:7023051"
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Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 994; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 994; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Oy 708 TGGGTCTGGGGGTGGTGGCATCTCCCCTAAAGGAAGTGGTCCCTCTGTGGCAAGTGATGA 767 Db 357 TGGGTCTGGGGGTGGTCGCCTCCCAAAGGAAAGACTGCCTCTCTGTGGCAAGTGATGA 416 Oy 768 AGTCTCCAGCTTTGCCTCAGCTCTCCCAGACAGAAAGACTGCGTCCTTTTCGTCGTTGGA 827	RESULT 10 AX834949 LOCUS DEFINITION AX834949 VERSION AX834949 VERSION AX834949 VERSION AX834949.1 GI:39921084 KEYWORDS SOURCE ORGANISM CORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURESS SOURCE ORGANISM RESULT 10 AX834949 AX834949 LOCATION AX8405 LOCATION AX84	Db 2178 CAGCAGAAGCATTTCTGTAACATGCGGCCGTCCTGCCGAGAGGGGCAGTTT 2237 2389 GCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAGTT 2448 [
RESULT 11 AK097671 AK	1368 CSTGTGGCCGGCAGTGTCCTGAGTACAGAAGGCAGGCGGCAGCCTCCCACTGCCCAGGCGGCGGCAGCCTCCCCACTGCCCAGGCGGCGGCAGGCGGCGAGCCTCCCACTGCCCAGGCGGCAGGCGGCGAGCCTCCCACTGCCCAGGCGGCGAGGCGAGCCAGGCAGG	Qy 1008 CTGCCAGGACCTGCTGCAGACTGCGTGAGTTTGCAGCCTGCATGCA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (04-701-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, 7el:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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/mol_type="mRNA"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6235)

Ohara,O., Nagase,T. and Nakajima,D.

Novel genes and proteins encoded by the genes
Patent: JP 2002345492-A 4 03-DEC-2002;
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JP 2002345492-A/4.
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Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.	Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Nakajama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,	Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Tanaki u Thoma of Control o	Shiobata', N., Sano, S., Moriya, S., Moriyama, H., Satob, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sudiyama A. Takemoto M. Kawakami B. Yamazaki M. Watanabe, K.	Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki N Actauka S Voshikawa V Matrumawa H Tohihara T	Kikawa, B., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S. (Thba, Y. Ishida, S. Ono Y. Takimorbi, S. Watanabe, S.	Ishil,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,	REFERENCE 1 AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sakino M. Ohayashi M. Nishi T. Shihahara T. Tanaka T.	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primares; Catarrhini; Hominidae; Homo.	to Homo Bapiens cell cycle checkpoint protein CHFR AK090948 AK090948.1 GI:21749208 AK090948.1 GI:21749208 oligo capping: fig [full insert segmence]	RESULT 13 AK090948 LOCUS AK090948 TETINA PLATE Clone RRAMY2022414 highly similar	Db 5585 TAATTTATAATTTACAAATTGAC 5607	5525 TAGGITTGGIGCTTATCTTCTAA	2519 GACGTACACAATATCCTGCTGCTGGGAAAACCACAGAGCATTTTATCTATTTTTAATTTTAA	Qy 2459 AGGGCAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAGTTTACAGCCTACAG 2518	Qy 2399 ACATTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAGTTTCAAGGGAGA 2458	Qy 2339 GACGAAGCCTTTCTGTAACATGCGGCCGTCCCGCCGAGAGGGGCAGTTTTGCTCTTTTGT.2398	5225 GCCGCAGCCCGCCCTCCTGGTGAGCGCTGGGCAGGGCTCGTGGTGGCATCAGCAGCAGA	Db 5167 GGGGTGACTCTTCTGTGGAGCTTTACCCTCTGAGTGAGACCCTCCCAGAGCCCCGGG 5224 Oy 2279 GGCCGCAGCCCCCCCCTCCTGGTGAGCGCCTCGTGGGCATCAGCAGCAGCAGA 2338

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and
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Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                  Patent: EP 1293569-A 160
Helix Research Institute
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                                TGACATGGAAAAAACATGTTGACCGAGAGCCTCGTGGCTCTCCAGCGGGGAGTGTTTCTGC
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to Ното
Sekine, M., Obayura
Sekine, M., Vamamoto, J.,
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AK054917.1 GI:16549547
oligo capping; fis (full insert sequence)
             Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y.,
                                                                                                                                 Homo.
                                                                                                                                                  Homo
                                                                                                              Eukaryota; Metazoa;
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sapiens cDNA FLJ30355 fis, clone BRACE2007688,
omo sapiens cell cycle checkpoint protein CHFR
                                                                                                                                 Bapiens
                                                                                                                                               sapiens (human)
                                                              Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
                                                                                                Eutheria;
                                                                                                Primates;
                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                  1558
                                                                                                                                                                                                                                                                                                                                                                 2661
                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                  mRNA.
                                                                                                                                                                                                                            PRI 30-JAN-2004
highly similar
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Nagahari, K., Murakami, K., Yasuda, T., Twayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, B., Omura, Y., Abe, K., Kamihara, K., Katsuta, M., Sato, K., Kikkawa, B., Omura, Y., Abe, K., Kamihara, K., Katsuta, M., Sato, K., Kikkawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanal, H., Kimata, M., Watanabe, M., Murakawa, K., Fujimori, K., Tanal, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Oxo, Y., Takdyuchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sandhia, Y., Sinuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimixu, F., Wakabe, H., Hishigaki, H., Watanabe, T., Goto, Y., Shimixu, F., Wakabe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Sasaki, M., Togashi, T., Nakajima, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs
                                       Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.
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/mol_type="mRNA" /db_xref="taxon:9606" organism="Homo sapiens"

/tissue_type="cerebellum" /clone_lib="BRACE2" /note="cloning_vector: pN clone="BRACE2007685" vector: pME18SFL3

Local Similarity 23.6%; Score Pred. NO. 0 B Length 2186;

Gaps

Gaps

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DEFINITION
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CQ719982
LOCUS
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                                                                                                                                                                    CQ719982 1085 bp DNA
Sequence 5916 from Patent WC02068579.
CQ719982 GI:42280839
             humanexons
thereof
                        Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and oth
                                                                                                                     Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                   ATATAATTTATAATTTACAAATTGAC 2661
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                                                                                       Eutheria;
                                                                                      Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
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Best Local Similarity
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                                                                                    Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 3663 07-FEB-2001; Research Association for Biotechnology (JP)
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Sequence 3663 from
AX868758
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                                                                                                                                                                                                                              Homo sapiens (human)
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PE Corporation (NY) (US)
Cocation/Qualifiers
1. 1085
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                          /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Pred. No. 4.1e-268;
0; Mismatches 0;
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JP 2002191363-A/3663.
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PC C12P21/
Primer for
                                                                                                                        HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/3663
PD 09-JUL-2002
PP 28-JUL-2000 JP 2000280990
PP 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 816)

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J. Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Irimer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 3663 09-JUL-2002;

HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)

DN 10-TU-2003
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                                                              C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00
mer for synthesizing full-length cDNA and use thereof FH 1
Location/Qualifiers
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/organism='Homo sapiens (human)'
Location/Qualifiers
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Pred. No. 3.2e-265;
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n cDNA and use thereof.
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Query Maest Lou Matches	FEATURES BOUICE	QY QY Db CY DB RESULT 20 BD148838 LOCUS DEFINITION ACCESSION VERSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	8 8 8 8 8 8 8 8
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PARENT: UP 200219183-A 8694 09-UUL-2002; HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191863-A/8694 PD 09-UUL-2002 PF 28-UUL-2000 JP 2000280990 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU PI SAITO, PI JUNICHI YAWAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAWATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC 10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers FT SOURCE JOURNAL SOURCE FH Key Location/Qualifiers Location/Qualifiers FT Location/Qualifiers Location/Qualifiers 1. 518 FT Location/Qualifiers 1. 518
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RESULT 23 AC127070 LOCUS DEFINITION ACCESSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	D Q D Q D Q D Q D Q D Q D Q D Q D Q D Q
AC127070 181012 bp DNA linear PRI 28 MAR-2003 ON Homo Sapiens 12 BAC RP11-66H11 (Roswell Park Cancer Institute Human BAC Library) complete sequence. M AC127070.10 GI:23343648 HTG. HOMO Sapiens (human) SM Homo sapiens (human) SM Homo sapiens (human) 1 (bases 1 to 181012) 2 (barron, P. Barbaria, J. Benton, J. Bimage, K. Blankenburg, K. Bonnin, D. Babbrooks, S.L. Amaratunge, H.C. Are, J.R., Ayele, M. Banks, T. Barbaria, J. Benten, J. Bimage, K. Blankenburg, K. Bonnin, D. Bouck, J. Benten, J. Burkett, C., Burrell, K.L. Byrd, N.C., Charler, M. Cavazos, S.R., Chacko, J., Chiavez, D., Carron, T.F., Carter, M. Cavazos, S.R., Chacko, J., Chiavez, D., Carron, T.F., Carter, M. Cavazos, S.R., Chacko, J., Chiavez, D., Carron, T.F., Carter, M. Cavazos, S.R., Chacko, J., Chiavez, D., Carron, T.F., Carter, M. Cavazos, S.R., Chacko, J., Chiavez, D., Carron, T.F., Carter, M. Cavazos, S.R., Chacko, J., Chiavez, D., Carron, T.F., Carter, M. Cavazos, S.R., Chacko, J., Chiavez, D., Carron, T.F., Carter, M. Cavazos, S.R., Chacko, J., Chiavez, D., Carron, T.F., Carter, M. Cavazos, S.R., Chacko, J., Chiavez, D., Carron, T.F., Carter, J., David, R., Guaratune, P., Hale, S., Hamilton, K., Han, J., Hartis, C., Hartis, K., Hart, M., Hayk, S., Hame, J., Galvis, J., Gabis, J	2305 GCTGGGCAGGGCTCGTGGTGGCATCAGCAGCAGAGACGAAGCCTTTCTGTAACATGCGC 2364

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Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are calculated and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-MAR-2003) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Sep 28, 2002 this sequence version replaced gi:22759174.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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Genetics, Baylor College
TX 77030, USA
                                                                                                                                                                                                                                                                          7:541-550) searches dbSTS, GDB, and
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of Medicine,
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COMMENT

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones reads with no ambiguities or 2 chemistries with a minimum of

mum of 2

e and

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clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
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QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: Location/Qualifiers

FEATURES

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                                                                                                                                                                                 complement (9483. .9665)
/rpt_family="L1ME1"
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complement (9339
                                                                                                                                                                                                                                                                                                              complement (7022. .777 /rpt_family="HERVL68"
                                                                                                                                                                                                                                                                                                                                                                                 complement (6437.
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complement(2108. .2205)
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complement(248. .802)
/rpt_family="AluY"
11820. .11846
/rpt_family="(TAAA)n"
                                        /rpt family="LIMC3"
[1539. .11819
                                                                  complement (11528.
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11248
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/rpt_family="L1PA16"
/^>>0 .94
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/db_xref="taxon:9606"
/chromosome="12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _family="Alu"
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ement (0/07
                            family="AluY"
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ement (6777
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                                                                                                                                                                                                                                                                                       name="RH44654"
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               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 181438)
                                                                                                                        AC023047.19 GI:9857509
HTG; HTGS_PHASE1; HTGS_DRAFT;
                                                                                                                                                                                            AC023047 181438 bp DNA 1
Homo sapiens chromosome 12 clone RP11-46H11,
SEQUENCE, 6 unordered pieces.
Abola, A.P., Bruno, D.,
                                                                                        Homo sapiens
                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGACTCTTCTGTGGAGCTTTTTACCCTCTGAGTGAGACCCTCCCCAGAGCCCCCGGGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCCTTTCTGTAACATGCGGCCGTCCCGCCGAGAGGGGCAGTTTTGCTCTTTTGTACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGGTGTTTTCACAGCCCCCTGAGGGGAAGGGACGCAGGGTCTCCGACAGGTGCTCTGGGG
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complement(12433...12741)
/rpt_family="AluSq"
complement(12742
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complement(12318.
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12282. .1231
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Conn, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 386; DB 9;
Pred. No. 2e-211;
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                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                              HTGS_FULLTOP; HTGS_ACTIVEFIN
Dela Rosa, M., Faulkner, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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3 DRAFT
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Venctor; 183mpls; X02513
Chemistry: Dye-primer; 1% of reads
Chemistry: Dye-primer; 1% of reads
Chemistry: Dye-primer; 1% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178770 bases at least Q40
Consensus quality: 178970 bases at least Q30
Consensus quality: 180370 bases at least Q20
Insert size: 180471; agarose-fp
Insert size: 180938; sum-of-contigs
Quality coverage: 10.7x in Q20 bases; sgarose-fp
Quality coverage: 9.7x in Q20 bases; sum-of-contigs.
NOTE: This is a 'working draft' sequence. It currently
consists of 6 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
truns of N, but the exact sizes of the gaps are unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (07-FEB-2000) DNA Sequencing and Technology Center,
Submitted University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 181438)
Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R., Morehouse, A. J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J., Yu, S. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will be preserved.
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Center clone name: RP11-46H11
Center clone name: Statistics
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note="assembly_name:Contig20"
                                    note="assembly_name:Contig19"
                                                                                   note="assembly_name:Contig18"
                                                                                                            23445. .38890
                                                                                                                            note="assembly_name:Contig17"
                                                                                                                                                       7110. .23344
                                                                                                                                                                       note="assembly_name:Contig16"
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                                                                                                                                                                                                                                                                  db_xref="taxon:9606"
chromosome="12"
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                                                                                                                                                                                                                                         clone="RP11-46H11"
                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                     7009: contig of 7009 bp in length
7109: gap of unknown length
23344: contig of 16235 bp in length
23444: gap of unknown length
38890: contig of 15446 bp in length
38990: gap of unknown length
55546: contig of 16556 bp in length
55646: gap of unknown length
103534: contig of 47888 bp in length
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                                                                                                                                                                                                                                                                                                                                                                          /Qualifiers
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Best Local Similarity
                                                                                                       AUTHORS
                                                                                                                                                                                                   ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 181438)

Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Mao, J., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Wilhelmy, J., Yu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                            181438 bp DNA li
Homo sapiens chromosome 12 clone RP11-46H11,
SEQUENCE, 6 unordered pieces.
AC023047
                                                                                                                                                                                                                       AC023047.19 GI:9857509
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAGTTTACAGCCTACAGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTATAATTTACAAATTGAC 2661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACACAATATCCTGCTGCTGGGAAAACCACAGCATTTTATCTATTTTTATTTTAATAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGCCTTTCTGTAACATGCGGCCGTCCCGCCGAGAGGGGCAGTTTTGCTCTTTTGTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGCCTTTCTGTAACATGCGGCCGTCCCCGCCGAGAGGGGCAGTTTTGCTCTTTTGTACAT
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clone_end:T7"
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Pred. No. 2e-211;
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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator Big Dye; 99% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178770 bases at least Q40
Consensus quality: 179776 bases at least Q30
Consensus quality: 180370 bases at least Q30
Consensus quality: 180370 bases at least Q30
Consensus quality: 180370 bases; agarose-fp
Insert size: 164471; agarose-fp
Quality coverage: 10.7x in Q20 bases; sum-of-contigs
Quality coverage: 9.7x in Q20 bases; sum-of-contigs
**NOTE: This is a 'working draft' sequence. It currently
consists of 6 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (07-FEB-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
2 (bases 1 to 181438)
Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N.,
Bruno,D., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
Glukhov,S., Hansen,N., Palm,C.J., Ramirez,D., Wilhelmy,J.,
Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
Yu,S. and Davis,R.W.
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On Aug 19, 2000 this sequence version replaced gi:9665109.
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------ Summary Statistics
Sequencing Vector: M13mpla; X02513
Chemistry: Dye-primer; 1% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: hum-info@sequence.stanford.edu
----- Project Information
Center project name: 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://sequence-www.stanford.edu/group/human/
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clone end:SP6"
103635 . 181438
/note="assembly_name:Contig21
clone_end:T7"
                                                                                                                           /note="assembly_name:Contig19" 55647. .103534
                                                                                                                                                                        /note="assembly_name:Contig18"
38991. .55546
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                          note="assembly_name:Contig17"
                                                                                                                                                                                                                                                                                                                                           'clone="RP11-46H11"
'clone_lib="RPCI human BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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7109: gap of unknown length
23344: contig of 16235 bp in length
23444: gap of unknown length
38890: contig of 15446 bp in length
38990: gap of unknown length
55546: contig of 16556 bp in length
55646: gap of unknown length
103534: contig of 47888 bp in length
103634: gap of unknown length
118438: contig of 77804 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                            chromosome="12"
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Best Local Similarity 100.0%; P
Matches 98; Conservative 0;
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Local Similarity 100.0%; Pred. No. 1e-113;
hes 218; Conservative 0; Mismatches 0; Indels 0;
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STS size:
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sqrmml10345 Human DNA (Sequenom)
tagged site.
BV180578
                                                                                                                                                                                                                                                                                                                                                                                       3595 John Hopkins Court, San Diego,
Tel: 18582029018
Fax: 18582029020
                                                                                                                                                                                                                                                                                                                                         Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Andreas Braun Pharmaceuticals division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 756)
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                                 GTAGCACAAATAATATAATTTATAATTTACAAATTGAC 2661
                                                                                             TATTTTTATTTTAATAGGTTTTGGTGCTTATCTTCTAATAAGATTTTAAATGTCACAAACT
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                GTAGCACAAATAATATAATTTATAATTTACAAATTGAC 629
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                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/clone lib="Human DNA (Sequenom)"
<1. .>756
                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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                                                                                                                                      Score 98; DB 11;
Pred. No. 3e-44;
0; Mismatches
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genomic, sequence
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BV168191/c
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AX385952/c
LOCUS
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BV168191
BV168191.1 GI:48001924
STS.
                                                                                                                                                                                                                                                                                                                                                           541 TAGCACAAATAATATAATTTATAATTTACAAATTGAC
                           Human genes and gene expression products
Patent: WO 0214500-A 880 21-FEB-2002;
CHIRON CORPORATION (US); Hyseq Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                Sequence 880 from Patent
AX385952
AX385952.1 GI:19579082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequenom, Inc.
3595 John Hopkins Court, San
Tel: 18582029018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 601)
                                                                                                         Escobedo, J., Randazzo, F.,
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: abraun@sequenom.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
/clone lib="Human DNA (Sequenom)"
<1...>601
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organism="Homo sapiens"
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                                                                                                       Garcia, P.D., Sudduth-Klinger, J., Lamson, G., Scott, E.M., Zhang, G.,
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                                                                                                                                                                                                                                                               617 bp
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1.1e-43;
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Kassam, A.,
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Mus musculus clone RP24-374B14, WAC118260

AC118260.3 GI:28604085

HTG; HTGS PHASE2; HTGS DRAFT.

Mus musculus (house mouse)

Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325
(bases 1 to 158897)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,

Boukhgalter, B., Brown, A., Camarrata, J., Campopiano, A., Chang, J.,

Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,

Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,

Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGAGTGTTTCTGCTGTCTGATTACAGAGTCACGGGAGACACCGTTCTGTGTTACTGCTGT
                                                                                                                                                                         1 (bases 1 to 158897)
Birren, B., Nusbaum, C. and Lande:
Mus musculus, clone RP24-374B14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S. Oligonucleotide library for detecting rna transcripts and s variants that populate a transcriptome Patent: WO 0210449-A 6220 07-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6220 from Pate CQ536585 CQ536585.1 GI:41502849
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                           Tandur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.2%; Score 60; DB 6; L. 100.0%; Pred. No. 2.8e-22;
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                                                                                                                                                                                               and Lander, E.
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WO0210449.
                                                                                                                                                                                                                                                                                                                                                                    DNA linear HTG WORKING DRAFT SEQUENCE.
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                                                                                                                                                                                                                                     Muridae;
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                                                                                                                                                                                                                                     Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (28-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 28, 2003 this sequence version replaced gi:28394919. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: 124782
Center clone name: 374 B 14
Center clone name: 374 B 14
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.96731
Consensus quality: 158848 bases at least Q40
Consensus quality: 158895 bases at least Q20
Consensus quality: 158897 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 158000; agarose-fp
Insert size: 158897; sum-of-contigs
Quality coverage: 12.6 in Q20 bases; agarose-fp
Quality coverage: 12.6 in Q20 bases; sum-of-contigs
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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    Genome Center

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COMMENT

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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg, A.C., Collins, F.S., Grouse, L.H., Derge, J.G.,
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Schnefer, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schnefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Muzny, D.M., Sodergaren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                    CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                       Submitted (31-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC049792
3194 bp mRNA linear ROD 30-JUN-Mus musculus checkpoint with forkhead and ring finger domains, (CDNA clone MGC:59419 IMAGE:6510480), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           assembly_fragment
                                                                                                                                  Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 3194)
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Cancer Agency,
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1 158897: contig of 158897 bp in length.
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/db_xref="taxon:10090"
/clone="RP24-374B14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-24 Male Mouse BAC"
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ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

AC087142.1 GI:11610868 HTG; HTGS PHASE1; HTGS DRAFT. Mus muscullus (house mouse) Mus muscullus RESULT 32 AC087142 LOCUS

DEFINITION

AC087142 321708 bp Mus musculus clone RP23-211L19,

DNA linear HTG WORKING DRAFT SEQUENCE,

HTG 09-DEC-2000 NCE, 65

unordered pieces.

밁

Query Match Best Local 9 Matches 3

Similarity

1.4%; ou 100.0%; Pr

Score 37; DB; Pred. No. 1.1: 0; Mismatches

DB 10; 1.1e-08;

Length 3194;

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0

Conservative

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ORIGIN
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27370049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy, Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Freatherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy L Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Mor Teika Olson, Diana Palmguist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
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                                                                                                  LLSPMAQTCLEEPQPSTSTSDLLPÄASTŠSTEPELTSAGQKHSSSGGGNTSISPKGR
SSLVANGELSSLSPVRQDKEASTSLLESKOHEELEPAKKKKKGJGELDTNLQLLVSGQ
RGNAQTSSEDVKOASVYGDKWESTLTCGICQDLLHDCVSLQPCHTFCAACYSGWER
SSLCPTCRCPVERICKNHILNNLVEAYLIQHPDKSRSEEDVRSMDARNKITQDMLQPK
VRRSFSDEEGSSEDLLEISDVDSESSDLSQPYLTCQCPEYRGAVQSLPCPVPESBL
GATLALGGERASTSASLFTAAPDYMCPLQGSHYICTCPQPMPDRRAEREDDFRVAPG
QCAVCLQPFCHLYWGCTRTGCFGCLAPFCELNLGDKCLDGYLNNNNYESDILKNYLAT
                                                                                                                                                                                                                                                                                                                                                            /translation="MELHGEEQPPPPQEPWGRLLRLGAEEDEPQILLWKREWTIGRRR
GCDLSPPSNKLVSGDHCKLTVDEISGEVTLEDTSTNGTVINKLQVVKKQTYPLQSGDI
IYLVVRKNEPEHNVAYLYESLSGKQSLTQDSLEANKEMWFHVTKDCSGPGQGDDPQVP
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undifferentiated limb containing undifferentiated limb
                                  RGLTWKSVLTESLLALQRGVFMLSDYRITGNTVLCYCCGLRSFRELTYQYRQNIPASE
LPVTVTSRPDCYWGRNCRTQVKAHHAMKFNHICEQTRFKN"
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/clone_lib="NIH_MGC_134"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAH49792.1"
/db_xref="GI:29437111"
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product="checkpoint with forkhead and ring finger
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db_xref="LocusID:231600"
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'db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 271436 bases at least Q40
Consensus quality: 288232 bases at least Q30
Consensus quality: 297606 bases at least Q20
Consensus quality: 297606 bases at least Q20
Consensus quality: 297606 bases at least Q20
Estimated insert size: 231000; agarcse-fp estimation
Estimated insert size: 315308; sum-of-contigs estimation
Quality coverage: 6.76 in Q20 bases; agarcse-fp estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 65 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary, Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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Center Code: JGI
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DOE Joint Genome Institute.
Sequencing of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (09-DEC-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center Project Name: 1818179
Center clone name: RPCI-23_211L19
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Summary Statistics
Consensus quality: 297593 bases at least Q40
Consensus quality: 310387 bases at least Q30
Consensus quality: 317713 bases at least Q20
Estimated insert size: 241000; agarose-fp estimation
Estimated insert size: 332616; sum-of-contigs estimation
                                                                                                                                                                                                       Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.iai Acc co
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HTG; HTGS_PI
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37; Conserv
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Mus musculus clone RP23-69F2, WORKING DRAFT
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                                                                                                                                                                    Project Information
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Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute.
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Mammalia; Eutheria; Rodentia;
1 (Dases 1 to 338116)
DOE Joint Genome Institute.
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/mol type="genomic DNA"
/db xref="taxon:10090"
/clone="RP23-211119"
/clone_lib="RPCI mouse BA
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PHASE1; HTGS_DRAFT.
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225667: contig of 11215 bp in 10
225767: gap of unknown length
245517: contig of 19750 bp in 10
245517: gap of unknown length
259483: contig of 13866 bp in 10
259583: gap of unknown length
259583: gap of unknown length
272039: contig of 12456 bp in 10
272139: gap of unknown length
272039: contig of 20130 bp in 10
272139: gap of unknown length
292269: contig of 29339 bp in 10
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RESULT 33 AC087159 LOCUS

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COMMENT

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Quality coverage: 8.79 in Q20 bases; agarose-fp estimation Quality coverage: 6.37 in Q20 bases; sum-of-contigs estimation. *NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as trues of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                        Rattus norvegicus clone CH230-314P18, ****, 7 unordered pieces.
  AC125898.3
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175: contig of 6713 bp in length
175: contig of 6561 bp in length
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175: contig of 10313 bp in length
175: contig of 6190 bp in length
175: contig of 6190 bp in length
175: contig of 10036 bp in length
177: contig of 10036 bp in length
177: contig of 10097 bp in length
177: contig of 10097 bp in length
177: contig of 13785 bp in length
177: contig of 13785 bp in length
177: contig of 13014 bp in length
177: contig of 13014 bp in length
177: contig of 5244 bp in length
177: contig of 5244 bp in length
177: contig of 14831 bp in length
178: contig of 16198 bp i
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/clone_lib="RPCI mouse BAC library 23"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
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    GI:25008623
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat)
Submitted (15-NOV-2002) Human Genome Sequencing Center, Departme of Molecular and Human Genetics, Baylor College of Medicine, Ont Baylor Plaza, Houston, TX 77030, USA On Nov 15, 2002 this sequence version replaced gi:23807727. The sequence in this assembly is a combination of BAC based reac and whole genome shotgun sequencing reads assembled using Atlas
                                                                                                                                                                                                                                                            Submitted (02-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 202792)
                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 202792) Worley, K.C.
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Rodentia;
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Sciurognathi; Muridae; Murinae;
                                                                                                                               nome Sequencing Center, Department Baylor College of Medicine, One
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a "working draft" sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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------ Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 166637 bases at least Q40
Consensus quality: 168395 bases at least Q30
Consensus quality: 168395 bases at least Q20
Estimated insert size: 172322; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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173948
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163997
170076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine Center code: BCM
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                       163997. .165926
/note="wgs end extension
clone end:Sp6"
167885. .170075
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clone_end:T7"
104416_.104486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Rattus norvegicus"
|mol_type="genomic DNA"
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s: gap of unknown length
s: contig of 6079 bp in length
s: gap of unknown length
r: contig of 3672 bp in length
r: gap of unknown length
l: contig of 3244 bp in length
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Query Match
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                                                                                                                                                                                                                                                 as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvImJ, C3H/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNI detection was carried out by SSAHA-SNP. 225,000 reads were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphism Structure in the Mouse Unpublished (2002)
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BV002855
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S208P6639RF11.TO 129S1/SvImJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BV002855.1
                                                                                                                                                                                                                                                                                                                                        annotated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STS size: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer B: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer A: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kersli@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 6172580903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 6172521477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 Charles Street,
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clone_end:Sp6"
172537. .173847
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/note="wgs_end_extension
clone_end:Sp6"
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clone_end:Sp6"
173948. .175125
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170176. .171329
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clone_end:Sp6"
                                                                                                    /db_xref="taxon:10090"
/map="+ 5 22-555 107871915-107872448"
/clone_lib="129S1/SvImJ"
                                                                                                                                                                mol_type="genomic DNA"
strain="12981/SvImJ"
                                                                                                                                                                                                          organism="Mus musculus"
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                                                                                  . >601
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  Score 32;
Pred. No.
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Mus musculus STS genomic,
DB 11; 1
7.1e-06;
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                   Length 601;
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100.0%;

Sequencing Center, Washington 4444 Forest Park Parkway, St.

Fouls

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RESULT 37
AC079981/c
LOCUS
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AUTHORS
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                                                                                                                                                                        Query Match
Best Local
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                                                                                                       2651 TACAAATTGACAAAAAAAAAAAAA 2679
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AC124951
AC124951.19
HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                The University Of Oklahoma
                                                                                                                                                                                                                                                                                                                                                                                                                                             OK 73019, USA
On Apr 30, 2004 this sequence version replaced gi:46358095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OK 73019, USA
4 (bases 1 to 124973)
Shaull,S., Lin,S., Dixon,R., May,G., Summer,L., Gonzales,B., Cook,D., Kim,D. and Roe,B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OK 73019, USA

3 (bases 1 to 124973)

Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L.,
Cook,D., Kim,D. and Roe,B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-7p23
   AC079981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (30-APR-2004) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-APR-2004) Department Of Chemistry The University Of Oklahoma, 620 Parrington Oval,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (20-JUN-2002) Department Of Chemistry The University Of Oklahoma, 620 Parrington Oval,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D. and Roe, B.A.
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                                                                                                                                                                                                                                                                                                                                                                                  Center code: UOKNOR
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                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                      /mol type="genomic DNA"
/db xref="taxon:3880"
/clone="mth2-7p23"
/clone_lib="Medicago truncatula BAC library H1"
                                                                                                                                                                                                                                                                                               /organism="Medicago truncatula"
/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                .124973
                                                                                                                                                                      1.1%;
                                                                                                                                                    Score 29; DB 8; Pred. No. 0.00
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hes 0;
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HTG 07-DEC-2000
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ORGANISM
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VERSION
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Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 129528 bases at least Q40
Consensus quality: 134760 bases at least Q30
Consensus quality: 137249 bases at least Q20
Insert size: 159000; agarose-fp
Insert size: 145550; sum-of-contigs
Quality coverage: 3.14 in Q20 bases; agarose-fp
Quality coverage: 3.59 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (20-SEP-2000) Genome Sequencing Center, Washingt University School of Medicine, 4444 Forest Park Parkway, 8 MO 63108, USA
On Dec 7, 2000 this sequence version replaced gi:11528609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens chromosome 16 clone RP11-21506, WORKING DRAFT SEQUENCE, 28 unordered pieces.
AC079981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing
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Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: H_NH0215006
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Waterston, R.H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                        10621
13359
                                                                                                                                                                                                        8163
10521
                                                  18588
21398
21498
                                                                                                                       15804
15904
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contig of 1440
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of 1647
                                                  unknown
of 4407
                                                                                    unknown
of 2810
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of 2584
                                                                                                                                                      unknown
of 2345
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of 2738
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of 2358
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of 1382
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774609
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77409
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             note="assembly_name:Contig36"
                                                                          note="assembly_name:Contig34"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="RP11-21506"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74608 gap of unknown length
74608 contig of 7923 bp in length
74708 gap of unknown length
75327 contig of 619 bp in length
75327 gap of unknown length
76074 contig of 647 bp in length
76174 gap of unknown length
81491 contig of 5317 bp in length
81591 gap of unknown length
88018 contig of 6427 bp in length
88018 gap of unknown length
88018 gap of unknown length
98670 contig of 10552 bp in length
98670 contig of 10552 bp in length
113277 contig of 14507 bp in length
113277 contig of 1449 bp in length
112726 gap of unknown length
127726 gap of unknown length
146516 contig of 14249 bp in length
146516 contig of 14790 bp in length
                                                                                                                                                                                                                                                                                                                                                                                     .10520
                                                                                                                                                                                                                                                                                         .18487
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contig of 4587
gap of unknown
contig of 5504
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contig of 6438
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contig of 712
gap of unknown
contig of 7923
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gap of unknown
contig of 4066
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             Similarity
ilarity 100.0%;
Conservative
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Pred. No.
DB 2; Length 146516;
0.003;
hes 0; Indels 0
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ACCESSION VERSION KEYWORDS RESULT 38
AC126634
LOCUS
DEFINITION AC126634 218226 bp DNA linear HTG 15-1 Rattus norvegicus clone CH230-138L3, WORKING DRAFT SEQUENCE HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat) AC126634.4 GI:25007898 HTG 15-NOV-2002

S

Matches

28;

0;

Mismatches

0

Gaps

0

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102453 ACAAATTGACAAAAAAAAAAAAAAAAA 102426

2652 ACAAATTGACAAAAAAAAAAAAAAAAAAA 2679

REFERENCE AUTHORS

SOURCE

ORGANISM

Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; (bases 1 to 218226)

RS Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguliano, D., Anylebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Anylebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Cardenas, V., Carter, K., Cavazos, I., Ceassar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Dayal, R., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Bscotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guarathe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, S., Huley, S., Hume, J., Idebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kally, S., Khan, Z., King, L., Kovar, C., Kowar, C., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Malloy, K., Mangum, A., Martin, K., Martin, R., Martine, E., Martin, R., Martine, R., Mar

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Milosavljevic, A., Miner, G., Minja, B., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nwaokelemeh, O., Okwuonu, G., Olarmpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L. L., Plazo, M., Quiroz, J., Rachlin, B., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Satsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Warren, J., Warren, R., Wei, X., White, F., Wang, Q., Wang, S., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Warren, R., Wak, S., Yen, J., Yoon, L., You, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhoo, S., Dunn, D., von, Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Reinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:22856032.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tcm.edu/projectes/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.
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                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.)
NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 218226)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: GZCL

Center clone name: CH230-13BL3

------ Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 206654 bases at least Q40

Consensus quality: 208130 bases at least Q20

Consensus quality: 208170 bases at least Q20

Estimated insert size: 213369; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine Center code: BCM
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REFERENCE AUTHORS TITLE

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AUTHORS

JOURNAL TITLE

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RESULT 39
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Best Local Similarity
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC111838.7 GI:25073437
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by the finished sequence as soon as it is available the accession number will be preserved.

1 218226: contig of 218226 bp in length.
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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100.0%; Pred. No. 0.0032;
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Rodentia;
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ne CH230-170E2,
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2, WORKING DRAFT
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HTG 19-NOV-2002

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                                                                                                                                                                                                                                                     Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Vilasana, D., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, J., Waldron, L., Walte, F., Wang, J., Wang, S., Warren, J., Wooden, H., Worley, K., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, P.N., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, P.N., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, P.N., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, P.N., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, P.N., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, P.N., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, P.N., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, P.N., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, P.N., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, P.N., Niederhausern, A., Weiss, R., Smith, P.N., Weiss, R., Smith, P.N., Weiss, R., Smith, P.N., Niederhausern, A., Weiss, R., Smith, P.N., Weiss, R., Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 19, 2002 this sequence version replaced gi:23265947. The sequence in this assembly is a combination of BAC based reads.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 228987)
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                                                                                                                                                                                                                                                                                                                                                      NOTE: Bstimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
1 228987: contig of 228987 bp in length.
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Center clone name: CH230-17022

Center clone name: CH230-17022

Assembly program: Phrap; version 0.990329

Consensus quality: 219472 bases at least Q40

Consensus quality: 221109 bases at least Q30

Consensus quality: 222076 bases at least Q20

Betimated insert size: 225540; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine Center code: BCM
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                                                                                                          /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                   clone="CH230-170E2"
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SOURCE
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       Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, G., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Devila, M. L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dumn, A., Durbin, K., Duval, B., Eaves, K., Eggan, A., Bsoctto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Perranadez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, M., Guevara, W., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Harlak, P., Haldun, S.L., Hodgson, A., Hogues, M., Harvey, Y., Havlak, P., Haldun, S.L., Hodgson, A., Hogues, M., Jackson, A., Jac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25009660.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hggc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome special contigs with sequence only contigs will be indicated in the feature
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                                                                                                 * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a 'working draft' sequence. If currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

be preserved.
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    271425
271525
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271424: contig of 271424 bp in length 271524: gap of unknown length 272554: contig of 1030 bp in length

    Genome Center

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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choppel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitcGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
                                                                                                                                                                                                                            Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 167166)
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Mus musculus clone RP24-511J14, WORKING DRAFT SEQUENCE, 4 unordered
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1. .274796
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db_xref="taxon:10116"
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273674: contig of 1020
273774: gap of unknown
274796: contig of 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Lander, E.
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassliev, H., Viel, R., VO, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* This record will be available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 165942 bases at least Q40
Consensus quality: 166212 bases at least Q30
Consensus quality: 166486 bases at least Q30
Consensus quality: 166486 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 168666; sum-of-contigs
Quality coverage: 12.9 in Q20 bases; agarose-fp
Quality coverage: 12.6 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be preserved.
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------ Project Information
Center project name: L11316
Center clone name: 511_J_14
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18166
                                                                                                                                                                                                                                 vector_side:right"
                                clone_end:T7
                                                                                          /note="assembly_fragment"
71984. .167166
                                                   note="assembly_fragment/
                                                                                                                                                          /note="assembly_fragment"
24969. .71883
                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-511J14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 24968: gap of 100 bp
71883: contig of 46915 bp in length
4 71983: gap of 100 bp
4 167166: contig of 95183 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                         clone_lib="RPCI-24 Male Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .167166
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REFERENCE
AUTHORS
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AC115904
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Best Local Similarity 100.0%;
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RS Birren, B., Nubbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Choepel, Y., Collymore, A., Cook, A., Cooke, B., Corum, B., DeArellano, K., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Doley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Jagos, B., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Jagos, B., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Jagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meddrim, J., Meneus, L., Mihova, T., Mlenga, V., Muzphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Spencer, B., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Wunan, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zodv, M., Whan, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zodv, M.
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Chang, J., Chapseller, B., Colins, S., Colymore, A., Cook, A., Cooke, P., DeArellano, K., Dear, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Giraham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kella, C., Larocque, K., Liu, G., Magos, B., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Travis, N., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Mu, X., Wyman, D., Ye, W.J., Young, G., Zaihoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Birren, B., Nusbaum, C. ar
Mus musculus chromosome
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Research, 320 Charles Street, Cambridge, MA 02141, 4 (bases 1 to 167938)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L24857
Center clone name: 472_P_22
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                                                                                                                                                                                                                                                                                                                                                                                                        /note="clone_boundary
clone_end:SP6
site:Mbol"
      /rpt_family="ORR1A2"
complement(3577. .3778)
                                                                                                                                                                                                                                                  /note="single clone coverage"
complement(356. .487)
/rpt_family="B4"
                                                                                                                                      complement(1408. .1518)
/rpt_family="PB1D7"
                                                                                                                                                                                                                                                                                                                                                                  rpt_family="L1M3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
|mol_type="genomic DNA"
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                                                                                                                                                                                                            rpt_family="ORR1D"
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chromosome="16"
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                                                          1.0%; Score 27; DB 10; Length 167938; larity 100.0%; Pred. No. 0.012; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                              complement(18012..18073)
/rpt family="tRNA-Ala-GCY"
complement(18073..18166)
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/rpt_family="B1_MM"
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 SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                              Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, sehttp://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-APR-2004)
Parkway, St. Louis, MO (
4 (bases 1 to 221753)
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On Jun 12, 2004 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUL-2004) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-JUN-2004)
Parkway, St. Louis, MO (
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Direct Submission
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Unpublished (2001)
2 (bases 1 to 221753)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                   MAPPING INFORMATION:
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Mammalia; Eutheria; Rodentia; Sciuro;
1 (bases 1 to 221753)
Harkins,R., Cotton,M. and Haglund,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: submissions@watson.wustl.edu
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25910. .25923
/rpt family="tRNA-Ala-GCY_"
25924. .25983
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7502. .7599
/rpt_family="B4"
7836. .8147
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8151. .9141
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25910. .25923
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24109
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19854. .1
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23968.
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11550. .1
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3319. .3555
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2694. .3089
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1610. .2005
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1390. _1475
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/db_xref="taxon:10090"
/chromosome="9"
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030. .7459
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                                                                                                                     1.0%; Score 27; DB 10; Length 221753; llarity 100.0%; Pred. No. 0.012; Conservative 0; Mismatches 0; Indels 0;
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54477. .54561
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AC123851.4
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Submitted (20-SEP-2002) Genome Sequencing Center,
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Shah,N., Kozlowicz,A. and Schatzkamer,K.
The sequence of Mus musculus BAC clone RP23-323K4
Unpublished (2001)
                                                                                                                                                                                                                                                       Submitted (14-FEB-2003) Genome Sequencing Center, Parkway, St. Louis, MO 63108, USA
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McPherson, J.D. and Waterston, R.H.
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                    Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics
Center project name: M_BA0323K04
                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu MAPPING INFORMATION: restriction digest. вее

SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

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This sequence is the entire insert
Location/Qualifiers
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/mol type="genomic DNA"
/db xref="taxon:10090"
/chromosome="16"
/map="16"
                                                                                         /rpt_family="B4"
8098. .8100
                /rpt_family="B4"
9680. .9812
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4850. .5007
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                                                               AL772311 234393 bp DNA linear ROI
Mouse DNA sequence from clone RP23-87P16 on chromosome
sequence.
AL772311
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                          HTG.
                                                     AL772311.19 GI:33412257
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/rpt_family="B4"
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19341. .20337
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|3506. .13579
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-87P16 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.

FOR further details see http://www.chori.org/bacpac/home.htm
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 239783)
                                                                                                                                        AC102564.3 GI:32490706
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Mus musculus (house mouse)
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Mus musculus clone RP23-210C12,
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                                                                                                                    Mus musculus
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This sequence was finished as follows unless otherwise noted: all
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Contact: humquery@sanger.ac.uk
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/mol_type="genomic DNA"
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/clone_lib="RPCI-23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CE 3 (bases 1 to 239783)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Docley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gadyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Liu, A., Mabbitt, R., MacLean, C., Kamat, A., Karatas, A., Kells, C., Liu, A., Mabbitt, R., MacLean, C., Mcdornald, P., Major, J., Manning, J., Matthews, C., McGarthy, M., Macdonald, P., Major, J., Manning, J., Matthews, C., McGarthy, M., Macdonald, P., Major, J., Manning, J., Mathews, C., McGarthy, M., Maclain, J., Meneus, L., Mihova, T., Mlenga, V., Murphy T., Naylor, J., Maching, D., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peerson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Spencer, B., Stange-Thomann, N., Stombas, M., Stubbs, M., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheepel, Y. Colangelo, M. Compounds, Collymore, A. Cooke, P. DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faxo, S., Cooke, P. DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faxo, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hilme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Liu, G., MacCean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., McDhue, J., Mihova, T., Mlenga, V., Murphy, T., Maylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Roy, A., Santos, R., Schauer, S., Schupback, R., Stauss, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travis, N., Triglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Direct Submission, M., Shimer, A., and Zody, M., Direct Submission, M., Shimer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 10, 2003 this sequence version replaced gi:22381552. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research. 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                Center project name: 119015

Center clone name: 210 C 12

Center clone name: 210 C 12

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 238594 bases at least Q40

Consensus quality: 238594 bases at least Q30

Consensus quality: 239154 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 239783)
                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 Charles Street, Cambridge, MA 02141,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nusbaum, C.
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                           ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                 AC129762
                                                                                                                                                                                                                                                      VERSION
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Best Local
                                                                                                                                                                                     ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       168024 САЛАТТСАСАЛАЛАЛАЛАЛАЛАЛАЛ 167998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2653 CAAATTGACAAAAAAAAAAAAAAAAA 2679
                                                                                                                  Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
                                                                                                                                                                                                                                                                                                              AC129762 266632 bp DNA linear HTG 09-
RATTUB CLORE CH230-42A2, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                               Rattue.
                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                      AC129762.3 GI:24635717
                                                                                                                                                                                                                                                                           AC129762
                                                                                                                                                                                                                                                                                              unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
                                                                                          (bases 1 to 266632)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 239283; sum-of-contigs
Quality coverage: 10.7 in Q20 bases; agarose-fp
Quality coverage: 9.5 in Q20 bases; sum-of-cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90332
90432
120456
120556
165385
165485
228024
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120556. .165384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
165485. .228023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-210C12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .239783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="RPCI-23 Female Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5588: contig of 5588 bp in length
5688: gap of 100 bp
90331: contig of 84643 bp in length
90431: gap of 100 bp
120455: contig of 30024 bp in length
120555: gap of 100 bp
165384: contig of 44829 bp in length
165384: gap of 100 bp
228023: contig of 62539 bp in length
228123: gap of 100 bp
239783: contig of 11660 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.0%; Score 27; DB 2; Length 239783;
100.0%; Pred. No. 0.012;
tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .90331
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TITLE
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COMMENT

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Cardenas, V., Chavez, D., Chen, G., Coale, N., Chen, C., Chen, C.,
                                                                                                                                                           On Nov 6, 2002 this sequence version replaced gi:23264331.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.lgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Molecular and Human Genetics,
Baylor Plaza, Houston, TX 77030,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 266632)
shotgun sequence only contigs will be indicated in the feature table.
                                                                                contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                    and separated
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RESULT 48
AC115400/c
                                DEFINITION
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                                                                                                                                                                                                                                                                         Matches 27;
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                           247436 CAAATTGACAAAAAAAAAAAAAAAAAAAA 247462
                                                                                                                                                                                                                         2653 CAAATTGACAAAAAAAAAAAAAAAA 2679
AC115400 269117 bp Rattus norvegicus clone CH230-59M6, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: GFFN

Center clone name: CH230-42A2

Center clone name: CH230-42A2

Center clone name: CH230-42A2

Center clone name: CH230-42A2

Assembly program: Phrap; version 0.990329

Consensus quality: 231272 bases at least Q40

Consensus quality: 231448 bases at least Q20

Consensus quality: 235932 bases at least Q20

Setimated insert size: 240545; sum-of-contige estimation

Estimated insert size: 240545; sum-of-contige estimation
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264710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="wgs_end_extension
clone_end:T7"
9336._.10170
                                                                                                                                                                                                                                                                                                                                                                                                                                           end_sequence:BH
263024. .264609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="wgs_contig"
complement(260236.
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clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                           /note="wgs_end_extension
clone_end:Sp6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           site:EcoRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="wgs_contig"
219565. .221299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/mol type="genomic DNA"
/mol type="genomic DNA"
/db xref="rtaxon:10116"
/clone="CH230-42A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .26663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264609: contig of 264609 bp in length 264709: gap of unknown length 266632: contig of 1923 bp in length.
                                                                                                                                                                                                                                                                                        1.0%; Score 27; DB 2;
100.0%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence:BH345974"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence:BH345972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Project Information
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                                                                                                                                                                                                                                                                      0; Mismatches
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                         DNA linear
, *** SEQUENCING
                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                    Length 266632;
                         HTG 08-OCT-2002
IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MZIN, METIE, WCEZKEY, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Angilano, D., Allen, H., Alsbrooks, S., Amin, A., Angilano, D., Anyalebechi, V., Avyadi, A., Avyadi, M., Baca, E., Badden, H., Ballen, C., Allen, H., Alsbrooks, S., Amin, A., Angilano, D., Allen, H., Alsbrooks, S., Amin, A., Angilano, D., Allen, H., Alsbrooks, S., Amin, A., Angilano, D., Allen, H., Alsbrooks, S., Allen, H., Barnstead, M., Banahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bladdwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bladdwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Brynn, R., Barnstead, M., Baryant, N., Buhay, C., Burch, P., Burch, R., Chen, Z., Chen, Z., Chu, J., Clavel, M., Cree, A., D'Souza, L., Cardenas, V., Carter, M., Carcia, R., Chen, X., Chen, Z., Chu, J., Chera, M., Cardenas, V., Carter, M., Digray, Dinh. H., Divya, K., Draper, H., Dugan, Rocha, S., Dum, A., Durkin, K., Duval, B., Baves, K., Egan, A., Eccotto, M., Egon, D., Garcia, M., 
Submitted (08-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 23, 2002 this sequence version replaced gi:22450411.
                                                                                                                                                                      Baylor Plaza, Houston, TX 77030, 3 (bases 1 to 269117)
                                                                                                                                                                                                                                                            Submitted (19-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 269117)
Worley, K.C.
                                                                                                                                                               Rat Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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AC115400.4 GI:23270024
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RESULT 49
AC131863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Rach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
    AC131863
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shotgun sequence only contigs will be indicated in the feature
                                                                                                               be preserved
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86696
167949
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265577
265677
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------ Project Information
Center project name: GNWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266794
266894
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                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                        /note="wgs_contig" 95067. .96319
                                                                                                                                                                                                                                                                                                                                           /note="wgg_contig"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
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/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                      note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .269117
                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="CH230-59M6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86595: contig of 86595 bp in length
86695: gap of unknown length
167948: contig of 81253 bp in length
168048: gap of unknown length
265576: contig of 97528 bp in length
26576: gap of unknown length
266793: contig of 1117 bp in length
266893: gap of unknown length
                                                                                                                                                                                                                         100.0%;
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100.0%; Pred. No.
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322833 bp
                                                                                                                                                                                                                            DB 2;
0.012;
  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in length
                                                                                                                                                                                                                                                 Length 269117;
  linear
HTG 23-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MIZIN, JMAILE, METZER, M.Lee., Abramzon, S. Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechil V., Ayogaji, A., Pyodaji, M., Baca, E., Baden, H., Balawin, D., Bandaranike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blatz, J., Blankenburg, K., Blyth, P., Brown, M., Chen, Z., Chu, J., Claecho, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claecko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claecho, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Diny, Y., Dinh, H., Divya, K., Draper, H., Duga, S., Denza, D., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bigene, C., Evale, A., Gracia, A., Gerter, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gunaratne, P., Haaland, M., Hamil, C., Hamilton, C., Hamilton, K., Harryy, Y., Raylak, P., Hawes, A., Henderson, N., Herrandez, J., Herrandez, R., Hines, S., Hladdin, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hally, S., Hume, J., Tidebird, D., Jackson, A., Hollins, B., Howells, S., Hally, S., Kally, S., Martin, R., Martin, R., Martin, S., Martin, R., Martin, R., Martin, R., Martin, S., Kally, S., Kall
Submitted (23-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                             Submitted (27-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 322833)
                                                                                                            Rat Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                        Rat Genome Sequencing Consortium.
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On Nov 23, 2002 this sequence version replaced gi:23322024.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently
consists of 10 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: GVEC
Center clone name: CH230-433M17
Center clone name: CH230-433M17
Center clone name: CH230-433M17
Consenbuy program: Phrap; version 0.990329
Consensus quality: 278235 bases at least Q30
Consensus quality: 278236 bases at least Q30
Consensus quality: 281659 bases at least Q20
Estimated insert size: 275728; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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318770: gap of unknown length
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318702: gap of unknown length
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Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment (s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr). AJ529544.1 GI.26797804 left border, T-DNA flanking sequence. Arabidopsis thaliana (thale cress) Arabidopsis thaliana Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A. Balzergue, S. of pre-insertion sites EMBO Rep. 3 (12), 1152-1157 (2002) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Arabidopsis thaliana T-DNA flanking sequence, left border, clone ATH529544 12446565 22363535 $\mathtt{T} ext{-}\mathtt{DNA}$ integration into the Arabidopsis genome depends on sequences (bases 1 to 444) Submission 444 bp DNA Samson, F., PLN 29-MAR-2003

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Abd75971 Human sof
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The present sequence is that of cDNA encoding the human mitotic checkpoint protein Chfr (see AAB20219) having a forkhead associated CC domain (FHA) and a ring finger domain. The protein is required for regulation of the transition of cells from prophase to metaphase during CC mitosis. It has ubiquitin-protein ligase activity. The Chfr checkpoint was evident in primary human cells, but was inactivated in 4 of 8 human CC cancer cell lines in U2OS cells, a mutation was identified, which caused CC a Val to Met amino acid substitution in the highly conserved C-terminal CC ys-rich region of the Chfr protein. In the absence of the Chfr CC checkpoint, cells subjected to mitotic stress condensed their chromosomes despite failing to separate their chromosomes. Chfr may monitor CC centrosome separation. Inactivation of the Chfr gene in human cancer is theorized to underlie the increased sensitivity of cancer cells to CC antimitotic drugs. Nucleic acids comprising the present sequence, or Sequences encoding at least amino acids 31-103, 303-346, 476-641 (or CC their antisense sequences) are claimed. The chfr cDNA was isolated from CC an expressed sequence tag database sequence for cDNAs with FHA motifs. Claimed methods of determining the tumourigenic potential of a cell comprise examining the cell for the presence of chfr nucleic acid comprise examining the presence of chfr nucleic acid of a cell. A composition which inhibits the biological activity of Chfr may comprise a ligand selected from an antibody or its fragment. The Chfr inhibit the activity of Chfr in a cancer cells. Cells inhibit the activity of Chfr in a cancer cells. A colditional antitumour therapies
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                                                                                                                              The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC conjected comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC specification and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers are also useful for the
CC chase easily without any specialised methods. AAH303166 to AAH328 and
CC chase easily without any specialised methods. AAH33629 to AAH33632 represent
CC coresent invention
CC coresent invention
    Query Match
Best Local Similarity
Matches 2133; Conser
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
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Ishii
                                                                                 Sequence
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length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
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Best Local Similarity
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P-PSDB; AAB83843.
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
coplynucleotide which comprises a 3'-end sequence complementary
to a
coligonucleotide comprises a 3'-end sequence, where the
coligonucleotide comprises a 1'-end sequence, where the
coligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence'3'-end sequence, where the
coligonucleotide comprises and the combination of
the 5'-end sequence'3'-end sequence, where the
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09-JUN-2000;
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Ishii
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cDNAs defined in the specification, and for the detection and/or
sis of the abnormality of the proteins encoded by the full-length
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3, Sugiyama
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AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

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Matches 1304; Conserv
                                                                                                                                                                                                                                                                                                                                                       The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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18-MAY-2000; 2000US-00577409.
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DB; ADM05831.
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J, Isono Y,
Yoshikawa T,
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
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R, Tamechika
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                              GENOME
                              SCI INC
               S.M.
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New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives. and

Claim 1; SEQ ID NO 22; 980pp; English.

cc pathological condition. Antibodies to the proteins can also be used in calleviating symptoms associated with the disorders and in diagnostic cc immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays cc (ELLSA). Disorders which are diagnosed or treated include autoimmune cc diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. carcollants of the breast or liver, cardiovascular disorders e.g. carciac cc arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, cr provided and formation of the content of the content, to maintain organs before cr preparate tissues and in chemotaxis. The polypeptides can also be used coast food additive or preservative to increase or decrease storage cc capabilities, fat content, lipid, protein, carbohydrate, vitamins, contents, contents, contents of the invention. Note: The sequence encodes a novel secreted protein of the invention. Note: The cc sequence data for this patent did not form part of the printed content. The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition.

밁 Ş 밁 δ 片 Ş 밁 Ś 밁 Ś 밁 Ś 밁 Ş 밁 S Query Match Best Local Sim Matches 765; 1190 1130 1070 1010 803 743 683 623 950 563 890 503 830 443 383 710 770 Similarity AGCGGATCTGTAAAAAACCACATCCTCAACAACCTCGTGGAAGCATACCTCATCCAGCATC CCCAGGATCAGGAGGATTTGGAGCCCGTGAAGAAAATGAGAGAAGAGAAGTGGGGACCTTG GGTCTGGGGGTGGTGGCATCTCCCCTAAAGGAAGTGGTCCCCTCTGTGGCAAGTGATGAAG CAGACAAGAGTCGCAGTGAAGAAGATGTGCAAAGTATGGATGCCAGGAATAAAATCACTC CTTGCTACTCGGGCTGGATGGAGCGCTCGTCCTGTGTCCTACCTGCCGCTGTCCCGTGG 1129 ACGTCAGAGCAGCGGCTGGGAAGCCAGACAAGATGGAGGAGACGCTGACATGCATCATCT ACGTCAGAGCAGCGGCTGGGAAGCCAGACAAGATGGAGGAGGACGCTGACATGCATCT ACCTGAACGGGCAGTTGTTGGTCGCACAACCGCGTAGAAATGCCCAAACCGTCCACGAGG CCCAGGATCAGGAGGATTTGGAGCCCCGTGAAGAAGAAAATGAGAGGAGGATGGGGACCTTG TCTCCAGCTTTGCCTCAGCTCTCCCAGACAGAAAGACTGCGTCCTTTTCGTCGTTGGAAC GGTCTGGGGGTGGCATCTCCCCTAAAGGAAGTGGTCCCTCTGTGGCAAGTGATGAAG CTTGCTACTCGGGCTGGATGGAGCGCTCGTCCCTGTCCTACCTGCCGCTGTCCCGTGG ACCTGAACGGGCAGTTGTTGGTCGCACAACCGCGTAGAAATGCCCAAACCGTCCACGAGG TCTCCAGCTTTGCCTCAGCTCTCCCAGACAGAAAGACTGCGTCCTTTTCGTCGTTGGAAC 28.6%; [larity 100.0%; Conservative (0; Score 765; DB 4; L Pred. No. 2.8e-273; 0; Mismatches 0; Length 1311; Indels 0 Gaps 1189 1249 1069 682 1009 742 862 802 622 949 562 688 502 829 442

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29-SEP-2000

29-SEP-2000

29-SEP-2000

29-SEP-2000

29-SEP-2000

02-OCT-2000

01-NOV-2000

01-NOV-2000

01-NOV-2000

01-NOV-2000
                                                                                                                                                                 New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders.
                                                                                                                                                                                                                                                   (ROSE/)
(RUBE/)
(BARA/)
                                                                                                                                                Claim 1; SEQ ID NO 22; 402pp; English.
                                                                                                                                                                                                                                   Rosen
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RUBEN S
BARASH
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2000US-0236367P.
2000US-0236368P.
2000US-0236369P.
2000US-0236309P.
2000US-0236309P.
2000US-0237039P.
2000US-0237039P.
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2000US-0237039P.
2000US-0237039P.
2000US-0237039P.
2000US-0241785P.
2000US-0241785P.
2000US-0244617P.
2000US-024968P.
2000US-0251868P.
2000US-0251868P.
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                                                                                                                                                                                                                                   Barash
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The invention relates to human novel polypeptides and their associated CC polynicelectides. The polypeptides and polynucleotides are useful in gene CC therapy for treating, inhibiting or preventing neural disorders, immune CC system disorders (e.g. systemic lupus crythematosus, rheumatoid arthritis cand multiple sclerosis), muscular disorders, respiratory diseases (e.g. CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g. CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage CC renal disease), hyperproliferative disorders (e.g. Hodykin's disease and CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and CC appendicitis), allergic reactions and conditions (e.g. asthma), blood CC related disorders (e.g. thrombosis, atherosclerosis and myocardial CC infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent NY

Sequence 1311 BP; 306 A; 359 C; 399 G; 239 T; 0 U; 8 Other;

멂 8

Length 1311;

밁 8 밁 8 S 문 S Query Match Best Local (Matches 890 830 443 770 710 765; Similarity ACCTGAACGGGCAGTTGTTGGTCGCACAACCGCGTAGAAATGCCCAAACCGTCCACGAGG CCCAGGATCAGGAGGATTTTGGAGCCCGTGAAGAAGAAAATGAGAGAGGAGATGGGGACCTTG TCTCCAGCTTTGCCTCAGCTCTCCCAGACAGAAAGACTGCGTCCTTTTCGTCGTTGGAAC TCTCCAGCTTTGCCTCAGCTCTCCCAGACAGAAAGACTGCGTCCTTTTCGTCGTTGGAAC GGTCTGGGGGTGGTGGCATCTCCCCCTAAAGGAAGTGGTCCCTCTGTGGCAAGTGATGAAG GGTCTGGGGGTGGTGGCATCTCCCCTAAAGGAAGTGGTCCCCTCTGTGGCAAGTGATGAAG CCCAGGATCAGGAGGATTTGGAGCCCGTGAAGAAGAAAATGAGAGGAGATGGGGACCTTG Conservative 28.6%; 0 Score 765; Pred. No. Mismatches 2.8e-273; 0 Indels 0, Gaps 562 889 502 829 442 949 769

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RESULT 10
ADA52592
ID ADA52
XX ADA52
XX 20-NO
DT 20-NO
DE Human
XX Cytog
KW Gene
KW infla
XX Infla
XX 19-MA
XX EP129
XX 12-MA
XX 14-SE
PR 24-JA
XX 14-SE
PR 24-JA
XX 18-SE
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                                              Isogai T,
Yamamoto
Seki N,
 WPI; 2003-395539/38
P-PSDB; ADA54231.
                                                                                                                                                                                                                                                                                                                         Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                      Human coding
                                                                                                                                                       14-SEP-2001; 2001JP-00328381.
24-JAN-2002; 2002US-0350435P.
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Yoshikawa
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                                                                Sugiyama
                                                                                                                                                                                                    2002EP-00006586
                                                                                                                                                                                                                                                                                                                                                                                      sequence,
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Hio Y, Otsuka K, Nagai
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                                              Masuho
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Best Local Similarity
Matches 863; Conserv
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                                                                                                                          AGAAGGGCAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAGTTTACAGCCTA
                                                                                                                                                                    TGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAGTTTCAAGGG
                                                                                                                                                                                    TGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGGAAAAGTTTTCAAGGG
                                                                                                                                                                                                                              AGAGACGAAGCCTTTCTGTAACATGCGGCCGTCCCGCCGAGAGGGGCAGTTTTGCTCTTT
                                                                                                                                                                                                                                                             AGAGACGAAGCCTTTCTGTAACATGCGGCCGTCCCGCCGAGAGGGGGCAGTTTTGCTCTTT
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New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
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NO 160; 205pp; English

The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease. 493 A; 555 C; 539 G; 599 T; 0 ₽, 0 Other;

TGACATGGAAAAACATGTTGACCGAGAGCCTCGTGGCTCTCCAGCGGGGAGTGTTTTCTGC TAACATCCCGTCCTGACTGCTACTGGGGCCCGTAACTGCCGCACTCAGGTGAAAGCTCACC TCCGTGAGCTGACCTATCAGTATCGGCAGAACATTCCTGCTTCCGAGTTGCCAGTGGCCG TGTCTGATTACAGAGTCACGGGAGACACCGTTCTGTTGTTACTGCTGTGGCCTGCGCAGCT TGACATGGAAAAACATGTTGACCGAGAGCCTCGTGGCTCTCCAGCGGGGAGTGTTTCTGC TCCGTGAGCTGACCTATCAGTATCGGCAGAACATTCCTGCTTCCGAGTTGCCAGTGGCCG TGTCTGATTACAGAGTCACGGGAGACACCGTTCTGTGTTACTGCTGTGGCCTGCGCAGCT Conservative 23.6%; 0; Score 633; DB 10 Pred. No. 1.8e-22 0; Mismatches Length 2186; Indels 2 Gaps 1915 1855 2035 1975 934 874 814 754

GCCCTGAGCAGCTTTCAGCACTGGAGGTGAAGAGAGGTGTTTTTAAAATACAGAGACAA ACACGTCAAGGTGTTTTCACAGCCCCCCTGAGGGAAGGGACGCAGGGTCTCCGACAGGTGC GCACGTCAAGGTGTTTTTCACAGCCCCCTGAGGGAAGGGAACGCAGGGTCTCCCGACAGGTGC GCCCTGAGCAGCTTTCAGCACTGGAGGTGAAGAGAGCGTGTTTTTAAAATACAGAGAGACAA ACGCCATGAAATTCAATCATATCTGTGAACAGACAAGGTTCAAAAACTAAGCATCCAGAG **ACGCCATGAAATTCAATCATATCTGTGAACAGACAAGGTTCAAAAACTAAGCATCCAGAG** 1114 1054 2155 1172 2215 2095 994

1412

1472

1352 2455 2395

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RESULT 11
AAHO6628
ID AAHO6628
AX AAHO
AX AAHO
AX AAHO
AX Huma
XX Huma
PF 29-J
PR 11-J
PR 12-J
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                                                                          The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at nucleotide which comprises a 5'-end sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 3'-end sequence, where the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. ANH03166 to ANH3628 and represent human amino acid sequences; and ANH3363 to ANH3632 represent flower invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, length cDNAs defined in the specification, and diagnosis of the abnormality of the proteins e
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3, Sugiyama
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; 99JP-00300253.
; 2000JP-00118776.
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T, Wakamatsu
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A, Nagai K,
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Ctsuki
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d for the detection and/or
encoded by the full-length
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Query Match

Sequence

816

BP;

182

A 17.8%; 216

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253

G; 162 T;

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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

Score 478;

멂 4.

Length 816; 3 Other;

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AAH06846
ID AAH
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                                                                                                              11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                Ota T,
Ishii
                                                                                                                                           29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                        28-JUL-2000;
                                                                                                                                                                                          07-FEB-2001.
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                                                                                                                                                                                                                                                  Human; primer;
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                                             2001-318749/34.
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, Sugiyama
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                                                                                                              99JP-00300253.
; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
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                                                               Nishikawa T,
T, Wakamatsu
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                                                              Hayashi K,
A, Nagai K,
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C, Otsuki
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Claim 1;
  SEQ
    ID NO
3681; 2537pp + Sequence Listing; English
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CC Insight cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an ollgonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC englementary strand of a polynucleotide which comprises a 5'-end
CC equence and an ollgonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence complementary to a
CC polynucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC planticularly full-length cDNAs. The primers set can be used in antisense therapy and in
CC particularly full-length cDNAs. The primers are useful for synthesising polynucleotides,
CC particularly without any specialised methods. AAH03166 to AAH328 and
CC cDNAs easily without any specialised methods. AAH03166 to AAH328 and
CC cDNAs easily without any specialised methods. AAH03166 to AAH3283 consent consent invention
CC coresent invention
CC coresent invention invention

Sequence 824 BP; 200 A; 203 C; 258 G; 161 T; 0 U; 2 Other;

Query Match Best Local Similarity

17.5%; 100.0%;

Score 468; Pred. No.

2.4e-163; DB 4;

Length 824;

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                                         TGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAACCGGGAACACAACGTGGCATACCT
                                                                TGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAACCGGAACACAACGTGGCATACCT
                                                                                       CAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCTTTACAGAC
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Human cDNA encoding a novel secreted protein, Seq IJ 483

cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; Human; immunosuppressi cardiant; vasotropic; preservative; immunosuppressive; antiarthritic; ss; antirheumatic; nt; vasotropic; cerebroprotective; nootropic; neuropr antiproliferative. neuroprotective; cytostatic;

Homo sapiens.

07-UIL-2000 07-UIL-2000 11-UIL-2000 11-UIL-2000 14-UIL-2000 26-UIL-2000 26-UIL-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 07-JUN-2000; 28-JUN-2000; 30-JUN-2000; 18-APR-2000; 19-MAY-2000; 16-MAR-2000; 17-MAR-2000; 17-JAN-2001; 2001WO-US001341.

14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 22-AUG-2000 22-AUG-2000 22-AUG-2000 23-AUG-2000 01-SEP-2000 08-SEP-2000 2000US-0189874P.
2000US-0198123P.
2000US-021515P.
2000US-021518867P.
2000US-0216880P.
2000US-0216880P.
2000US-0218890P.
2000US-0218890P.
2000US-0218890P.
2000US-0224519P.
2000US-0225213P.
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2000US-0225213P.
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2000US-0225214P.
2000US-0225214P.
2000US-0225214P.
2000US-0225214P.
2000US-0225267P.
2000US-022575P.
2000US-023575P.
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2000US-023575P.
2000US-023575P.
2000US-023144P.
2000US-023144P.
2000US-023144P.
2000US-0231414P.

RESULT 13
AAS26304
ID AAS2
XX
AC AAS2
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AC AAS2
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AC AAS2
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standard;

CDNA;

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ВP

07-NOV-2001 AAS26304; AAS26304

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                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC in diagnosing a pathological condition or susceptibility to a CC pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiovascular disorders e.g. corneal infections caused by Dacteria, viruses and fungi and ocular disorders e.g. corneal infection, CC and many other disorders listed in the specification. The polypeptides CC can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, procean, carbohydrate, vitamins, cc minerals, cofactors and other mutritional components. The present CC sequence encodes a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
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Matches 455
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06-DEC-2000;

06-DEC-2000;

08-DEC-2000;

08-DEC-2000;

08-DEC-2000;

08-DEC-2000;

11-DEC-2000;

11-DEC-2000;

15-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives.
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DB; AAU16317.
254
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 TTCTGATGAAGAAGGAGTTCAGAGGACCTGCTGGAGCTGTCAGACGTTGACAGTGAGTC
                      TTCTGATGAAGAAGGAGTTCAGAGGGACCTGCTGGAGCTGTCAGACGTTGACAGTGAGTC
                                                                   CGTGGAAGCATACCTCATCCAGCATCCAGACAAGAGTCGCAGTGAAGAAGATGTGCAAAG
                                                                                                                                                                 CGTGGAAGCATACCTCATCCAGCATCCAGACAAGAGTCGCAGTGAAGAAGATGTGCAAAG
                                                                                                                                                                                                                    GTGTCCTACCTGCCGCTGTCCCGTGGAGCGGATCTGTAAAAACCACATCCTCAACAACCT
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2000US-0256719P.
2000US-0251479P.
2000US-0251856P.
2000US-0251868P.
2000US-0251869P.
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2000US-0254099P.
2000US-0254097P.
2001US-0259678P.
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1.6e-158;
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01-NOV-2000

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2000US-024926P.
2000US-024929P.
2000US-024929P.

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RESULT 14
ABX73645
ID ABX73
AX ABX73645
XX ABX73645
XX ABX73645
XX Human
XX Human
XX Human
XX Human
XX Gast
XW haer
XX Carr
XW haer
XX US2
XX US2
XX 11
PR 11
PR 28
PR 28
PR 21
PR 21
PR 21
PR 11
PR 21
PR 2
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  14 AUG-2000

20 AUG-2000

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01 SEP-2000

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05 SEP-2000

25 SEP-2000

27 SEP-2000

29 SEP-2000

29 SEP-2000
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26-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene; ds; neural disorder; immune system disorder; renal disord muscular disorder; respiratory disease; reproductive disorder; gestrointestinal disorder; pulmonary disorder; cardiovasquar disorder hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1464
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0; 2000US-0217487P.
0; 2000US-0217496P.
0; 2000US-0218299P.
0; 2000US-0229513P.
0; 2000US-022567P.
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0; 2000US-0225447P.
0; 2000US-022543P.
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TATGGATGCCAGGAATAAAATCACTCAAGACATGCTGCAGCCCAAAGTCAGGCGGTCTTT CGTGGAAGCATACCTCATCCAGCATCCAGACAAGAGTCGCAGTGAAGAAGATGTGCAAAG CGTGGAAGCATACCTCATCCAGCATCCAGACAAGAGTCGCAGTGAAGAAGATGTGCAAAG

193 1223 133 1163

1283

253

1343

1164

134

1104

GTGTCCTACCTGCCGCTGTCCCGTGGAGCGGATCTGTAAAAACCACATCCTCAACAACCT

73

14

74

1284

TTCTGATGAAGAAGGGAGTTCAGAGGACCTGCTGGAGCTGTCAGACGTTGACAGTGAGTC

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Best Local Sim
Matches 455;
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29-SEP-2000;
02-OCT-2000;
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21-OCT-2000;
20-OCT-2000;
21-OCT-2000;
01-NOV-2000;
01-NOV-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                           The invention relates to human novel polypeptides and their associated polypucleotides. The polypeptides and polypucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders; immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and eukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial human novel columnia of the 
                                                                                                                                                       Sequence 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular orenal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 483; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-147444/14.
P-PSDB; ABU55385.
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                                                                                     Similarity
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RUBEN
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                                                                                                                                                                                                polynucleotides of the invention
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7 2000US - 0236802P.
7 2000US - 0237637P.
7 2000US - 0237037P.
7 2000US - 0237039P.
7 2000US - 0237039P.
7 2000US - 0237040P.
7 2000US - 0240960P.
7 2000US - 0241785P.
7 2000US - 0241869P.
7 2000US - 024461P.
7 2000US - 024461P.
7 2000US - 024461P.
7 2000US - 024461P.
7 2000US - 0251866P.
7 2000US - 0251869P.
                                                             Conservative
                                                                                                                                                     BP; 145 A; 214 C; 197 G; 123 T; 0 U; 14 Other;
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                                                                                                          17.0%;
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                                                                                Score 455; DB 8; L
Pred. No. 1.6e-158;
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                                                                Mismatches
                                                           0;
                                                                                                     Length 693
                                                                Indels
                                                             0;
                                                           Gaps
                  1103
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RESULT 15
AAH1189/c
ID AAH118
XX AAH118
XX AAH118
XX Human
DE Human;
XX Human;
XX EP1074
XX EP1074
XX 29-JUL
PR 27-AUG
PR 11-AUG
PR 27-AUG
PR 02-JUL
XX Ota T,
PI Ishii
XX PR WPI; 2
XX PR WPI; 2
XX PR WPI; 2
XX PR Ota T,
PI Ishii
XX PR Undan;
XX PR Ota T,
PI Ishii
XX PR Ota T,
PI Glagnc
PT CLaim
XX PR Ota T,
PI Glagnc
CC Inngli
CC Compli
CC Onuclec
CC Oligor
CC Sequen
CC Sepace
CC CLAim
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length cDNAs defined in the specification, where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises a 1-end sequence, where the coligonucleotide comprises a 1-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence 3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota T, :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1999; 99JP-00248036.
27-AUG-1999; 99JP-0030253.
11-JAN-2000; 2000JP-00118776.
02-MAX-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH11859 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 full-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai T,
3, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection; diagnosis; antisense therapy; gene therapy;
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T, Wakama
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A, Nagai K,
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C, Otsuki
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention
                                                                                    2545
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                                                      143
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83
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GATTTAAATGTCACAAACTGTAGCACAAATAATATAATTTATAATTTACAAATTGAC
                GATTTAAATGTCACAAACTGTAGCACAAATAATATAATTTATAATTTTACAAATTGAC 2661
                                                      ANAACCACAGCATTTTATCTATTTTTATTTTAATAGGTTTGGTGCTTATCTTCTAATAA
                                                                      AAAACCACAGCATTTTATCTATTTTTTATTTTAATAGGTTTTGGTGCTTATCTTCTAATAA
                                                                                                               TCAGGAGAAGGGAGCATAAGTTTACAGCCTACAGGACGTACACAATATCCTGCTGCTGGG
                                                                                                                                       TCAGGAGAAGGGAGCATAAGTTTACAGCCTACAGGACGTACACAATATCCTGCTGCTGGG
                                                                                                                                                                       AAAAGTCTGTTTTCAGGAAAAGTTTCAAGGGAGAAGGGCAAGTTTATCAAAAACATTGTT
                                                                                                                                                                                        AGAAGTCTGTTTTCAGGAAAAGTTTCAAGGGAGAAGGGCAAGTTTATCAAAAACATTGTT
                                                                                                                                                                                                                                              CGTCCCGCCGAGAGGGGAGTTTTGCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGC
                                                                                                                                                                                                                                                                                        GCTGGGCAGGGCTCGTGGCATCAGCAGCAGAGACGAAGCCTTTCTGTAACATGCGGC
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                                                                                                                                                                                                                                                                                                                                                  AGGGAAGGGACGCAGGTCTCCGACAGGTGCTCTGGGGGTGACTCTTCTGTGGAGCTTTTT
                                                                                                                                                                                                                                 CGTCCCGCCGAGAGGGGCAGTTTTGCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGC
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99.8%;
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Pred. No. 8.9e-148;
0; Mismatches 1;
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27
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AAA44336 standard; cDNA; 575 ВP

21-AUG-2000 (first entry)

Human secreted expressed sequence tag SEQ Ħ NO:911.

ARBSULT 16
AAA44336
ID AAA44
XX AAA44
XX 21-AU
DT 21-AU
XX Human
X expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoletic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antiidabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; nootropic; antiparkinsonian; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; parkinson's disease; huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; Human; mouse; chicken; rat; secreted expressed sequence depression; psoriasis; ss

WO200021991-A1

20-APR-2000.

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KESULT 17
AAS26143
                                                                                                                                                                                                                                                                                                                                                                                                                                               CC AAA43426 to AAA45925 represent specifically claimed secreted expressed CC sequence tags (sESTs), isolated from human, mouse, chicken and rat tissue Sources. The sESTs can have a range of activities depending on the CC tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; CC haemostactic; thrombolytic; antifulamentory; cytostatic; antipacterial; antidiabetic; antistathmatic; vulnerary, antipacterial; CC extended for gene therapy and in vaccines include pressant. The sESTs can be cused for gene therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA C molecules which correspond to the sESTs. Proteins encoded by the sESTs care useful as says for determining biological activity and raising c antibodies. They may be useful for treatment of autoimmune disorders (C (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (C (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation c disorders (Alaheimer's, Parkinson's, Huntington's disease, stroke), coagulation c disorders (Alaheimer's, Parkinson's, Huntington's disease, stroke), coagulation and cord sporiasis. AAA45926 to AAA45931 represent linker variants which are given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 575 BP; 124 A; 168 C; 165 G; 118 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 437; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-317938/27
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                                                                                                              1116
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                           CACGTTCTGCGCGGCTTGCTACTCGGGCTGGATGGAGCGCTCGTCCCTGTGTCCTACCTG
                                                                                                                                                                                                                AACCGTCCACGAGGACGTCAGAGCAGCGGCTGGGAAGCCAGACAAGATGGAGGAGACGCT
                                                                                                                                                                                                                                                                                                             AGATGGGGACCTTGACCTGAACGGGCAGTTGTTGGTCGCACAACCGCGTAGAAATGCCCA
                                                                                                                                                                                                CACGTTCTGCGCGGCTTGCTACTCGGGGCTGGATGGAGCGCTCGTCCCTGTGTCCTACCTG
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Treacy M,
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Bowman MR;
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Pred. No. 5.6e-96
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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preservative;
                                                                                                                                    Human; immunosuppressive; antiarthritic; ss; antirheumatic;
                                                                                                                                                                        Human
                                                                                                                                                                                                        07-NOV-2001
                                                                                                                                                                                                                                           AAS26143;
                                                                                                                                                                    cDNA encoding a novel secreted protein,
                                                                                                                                                                                                        (first entry)
antiproliferative.
                                                                                                                                                                    Seq
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cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral isohaemia; angiogenesis; nervous system disorder; cerebral isohaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; cytostatic;

14 AUG-2000 22 AUG-2000 22 AUG-2000 22 AUG-2000 22 AUG-2000 23 AUG-2000 01 SEP-2000 01 SEP-2000 01 SEP-2000 01 SEP-2000 05 SEP-2000 06 SEP-2000 08 SEP-2000 08 SEP-2000 08 SEP-2000 11-JUL-2000 11-JUL-2000 14-JUL-2000 26-JUL-2000 26-JUL-2000 26-JUL-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 07-JUL-2000; 16-MAR-2000; 17-MAR-2000; 18-APR-2000; 19-MAY-2000; 17-JAN-2001; WO200155322-A2 Homo sapiens. 2000US-0186350P.
2000US-019874P.
2000US-0199076P.
2000US-019813P.
2000US-0209467P.
2000US-0216647P.
2000US-0216649P.
2000US-0216963P.
2000US-0217496P.
2000US-0224518P.
2000US-0224519P.
2000US-0225264P.
2000US-02252714P.
2000US-0225275P.
2000US-0225275P.
2000US-022575P.
2000US-023575P.
2000US-023575P.
2000US-023743P.
2000US-0231244P.
2000US-0231244P. 2000US-0179065P 2000US-0180628P 2000US-0184664P 2001WO-US001341

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AAS26143 standard; cDNA; 357 BP

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21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
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29-SEP-2000
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20-OCT-2000
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2000US-023364P
2000US-0233064P
2000US-0233065P
2000US-0234274P
2000US-0234274P
2000US-0234998P
2000US-0235484P
2000US-0235834P
2000US-0235836P
2000US-0236367P
2000US-0236369P
2000US-0236369P
2000US-0246478P.
2000US-0246523P.
2000US-0246525P.
2000US-0246528P.
2000US-0246528P.
2000US-0246610P.
2000US-0246611P.
2000US-0246611P.
2000US-0246611P.
2000US-0249208P.
2000US-0249210P.
2000US-0249211P.
2000US-0249218P.
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2000US-0249264P.
2000US-0249264P.
2000US-0249299P.
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2000US-0241221P.
2000US-0241785P.
2000US-0241786P.
2000US-0241786P.
2000US-0241808P.
2000US-0241809P.
2000US-0241829P.
2000US-0244617P.
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2000US-0236802P.
2000US-0237037P.
2000US-0237038P.
2000US-0237039P.
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Matches 267
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01-DEC-2000
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267; Conserv
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WPI; 2001-488783/53.
P-PSDB; AAU16156.
                                                                        HUMAN GENOME
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2000US-0256719P.
2000US-0251479P.
2000US-0251856P.
2000US-0251868P.
2000US-0251868P.
2000US-0251989P.
2000US-0251989P.
2000US-0254097P.
2001US-0259678P.
                                                                                                                                                                                                                                                   2000US-0249300P.
2000US-0250160P.
2000US-0250391P.
2000US-0251030P.
                                         sc,
                                                                        SCI INC
                                           MS
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New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives. and

SEQ ID NO 322; 980pp; English.

The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a CC pathological condition. Antibodies to the proteins can also be used in CC alleviating symptoms associated with the disorders and in diagnostic CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac carrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac carrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, CC neoplasms of the breast or liver, cardiovascular disorders e.g. corneal infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, CC and many other disorders listed in the specification. The polypeptides CC can also be used to aid wound healing and epithelial cell proliferation, CC transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used casabilities, fat content, lipid, protein, carbohydrate, vitamins, CC minerals, cofactors and other nutritional components. The present CC sequence encodes a novel secreted procein of the invention. Note: The gourse and the printed content of t

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CCTTCCCCAGCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAAT
                       CCTTCCCCAGCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAAT
                                                                               CGCACGTCCTCCTGAGGAAGCGGGAGTGGACCATCGGGCGGAGACGAGGTTGCGACCTTT
                                                                                                    CGCACGTCCTCCTGAGGAAGCGGGAGTGGACCATCGGGCGGAGACGAGGTTGCGACCTTT
                                                                                                                                                                AGTCGCCGCCGCCGCAGCCCTGGGGAACGGCTCCTGCGTCTGGGCGCGGAGGAGGGCGAGC
                                                                                                                                                                                   AGTCGCCGCCGCAGCCCTGGGGACAGCTCCTGCGTCTGGGCGCGGAGGAGGAGGGCGAGC
                                                                                                                                                                                                                                               TCCGGGTTCGGCGCGGCGGCGATGTGAATCCCGATGGAGCGGCCCGAGGAAGGCAAGC
                                                                                                                                                                                                                                                                         TCCGGGTTCGGCGCGGGGCGGGGGATGTGAATCCCGATGGAGCGGCCCGAGGAAGGCAAGC
                                                                                                                                                                                                                                                                                                                          10.0%; Silarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                          Score 267; DB; Pred. No. 6.5
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DB 4; I 6.5e-89;

Length 357;

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RESULT 18
ABX73484
IDX73484
IDX73484
IDX73484
IDX73484
IDX ABX73
IDT 18-MA
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26-JUL-2000

26-JUL-2000

14-AUG-2000

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30-AUG-2000

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03-SEP-2000

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07-SEP-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2001;
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haemostatic; antiarteriosclerotic.
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                                                                                            2000US-0224518P
2000US-0224519P
2000US-022526P
2000US-0225270P
2000US-0225758P
2000US-0225758P
2000US-0225875
2000US-0226868P
2000US-0226868P
2000US-0229345P
2000US-0229345P
2000US-0229345P
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2000US-0239345P
2000US-0234274P
2000US-0234274P
2000US-0236367P
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2000US-0216486P
2000US-021664PP
2000US-0217487P
2000US-0217496P
2000US-0218290
2000US-0218290
2000US-0220964P
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RESULT 19
AAS26563
ID AAS26

AAS26563 standard; cDNA; 354

BP.

244 295 235

184

175 64

124

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AAS26563;

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                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human novel polypeptides and their associated CC polymucleotides. The polypeptides and polymucleotides are useful in gene cc therapy for treating, inhibiting or preventing neural disorders, immune cc system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. cand multiple sclerosis), muscular disorders, respiratory diseases (e.g. casal vestibulitis, nasal polyps and sinustis), reproductive disorders (c.g. systemital disorders, pulmonary disorders, cardiovascular disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left cheart syndrome), renal disorders (e.g. acute kidney failure and end-stage crenal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood crelated disorders (e.g. thrombosis, atherosclerosis and myocardial confarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent conditions (e.g. specific shock) and cancerous diseases.
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 267; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
17-NOV-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-147444/14.
P-PSDB; ABU55224.
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 245
                               296
                                                              185
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                                                                                                                                                                                                                                                                                                                                                                             357
                                                                                                                                             CGCACGTCCTCCTGAGGAAGCGGGAGTTGGACCATCGGGCGGAGACGAGGTTGCGACCTTT
                                                                                                                                                                                                         AGTCGCCGCCGCCGCAGCCCTGGGGACCGCTCCTGCGTCTGGGCGCGGAGGAGGGCGAGC
                                                                                                                                                                                                                                                                         TCCGGGTTCGGCGCGGGGCCGGGGATGTGAATCCCCGATGGAGCGCCCCGAGGAAGGCAAGC
CAGGTCAGGTGACACTGGAAGATACCA
                             CAGGTCAGGTGACACTGGAAGATACCA
                                                              CCTTCCCCAGCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAAT
                                                                              CCTTCCCCAGCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAAT
                                                                                                                                                                                                                                                    SEQ ID NO
                                                                                                                         CGCACGTCCTCAGGAAGCGGGAGTGGACCATCGGGCGGAGACGAGGTTGCGACCTTT
                                                                                                                                                                                       AGTCGCCGCCGCAGCCCTGGGGACGGCTCCTGCGTCTGGGCGCGGAGGAGGGCGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 2000US-0240960P.
; 2000US-0241785P.
; 2000US-0241809P.
; 2000US-0244617P.
; 2000US-0249299P.
; 2000US-0251868P.
; 2000US-0251868P.
                                                                                                                                                                                                                                                                                                               10.0%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                             B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402pp; English
                                                                                                                                                                                                                                                                                                            Score 267; DB 8; L; Pred. No. 6.5e-89; Wismatches 0;
                                                                                                                                                                                                                                                                                                                                                                             66
271
                             322
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                                                                                                                                                                                                                                                                                                                                                                             2 Other;
                                                                                                                                                                                                                                                                                                                                           Length 357;
                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                             Gaps
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31-JAN-2000
24-FEB-2000
24-FEB-2000
24-FEB-2000
16-FAR-2000
17-MAR-2000
19-FAX-2000
28-JUN-2000
28-JUN-2000
27-JUL-2000
27-JUL-2000
26-JUL-2000
14-JUL-2000
14-JUL-2000
14-JUL-2000
14-AUG-2000
16-AUG-2000
17-AUG-2000
16-AUG-2000
17-AUG-2000
17-AUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding a novel secreted
2000US-0179065P

2000US-0184664P

2000US-0184664P

2000US-0184664P

2000US-019467P

2000US-0199076P

2000US-029467P

2000US-0214886P

2000US-021647P

2000US-021647P

2000US-021648P

2000US-021890P

2000US-021890P

2000US-0225214P

2000US-0225214P

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2000US-0225214P

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2000US-0225214P

2000US-0225266P

2000US-0225270P

2000US-022547P

2000US-022547P

2000US-0225479P

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2000US-0225479P

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2000US-0225479P

2000US-02257579P

2000US-0235754P

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2000US-023343P

2000US-0233444P

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14-SEP-2000
25-SEP-2000
25-SEP-2000
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26-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
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02-OCT-2000
02-OCT-2000
03-NOV-2000
01-NOV-2000
08-NOV-2000
01-NOV-2000
08-NOV-2000
01-NOV-2000
2000US-023198P

2000US-023198P

2000US-0232398P

2000US-02332401P

2000US-0233063P

2000US-0233063P

2000US-023429P

2000US-023429P

2000US-023429P

2000US-0235834P

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2000US-0235834P

2000US-023632P

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2000US-024924P

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                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated nucleic acid molecules and their cencoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, corabbite, goats, horses, cate, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a condition antibodies to the proteins can also be used in condition antibodies to the proteins can also be used in condition associated with the disorders and in diagnostic conditions associated with the disorders and in diagnostic conditions are diagnosed or treated include autoimmune conditions. The proteins can also be used in conditions are diagnosed or treated include autoimmune consists of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, construity other disorders e.g. cerebral ischaemia, angiogenesis, consolus many other disorders e.g. cerebral ischaemia, angiogenesis, consolus also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before can also be used to aid wound healing and epithelial cell proliferation, to respectate tissues and in chemotaxis. The polypeptides can also be used as food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, ceapabilities fat content, lipid, protein, carbohydrate, vitamins, ceapabilities and content, lipid, protein of the invention. Note: The sequence data for this patent did not form part of the printed
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Best Local S
Matches 238
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05-DEC-2000; 2000US-02519P.
06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251999P.
11-DEC-2000; 2000US-025199P.
11-DEC-2000; 2000US-0254997P.
15-DEC-2000; 2000US-0254997P.
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01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 742; 980pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions
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                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                          CGGAACACAACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGACACA 482
                                                                                                                                                                       TGACACTGGAAGATACCAGCACCAGTGGAACAGTGATTAACAAGCTGAAGGTTTAAGA
                                                                                                                                                                                                          TGACACTGGAAGATACCAGCACCAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGA
                                                                                                                                                                                                                                                         GCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGGTCAGG
                                                                                                                                                                                                                                                                                                 GCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGGTCAGG
CGGAACACAACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGACACA 288
                                                                                    AGCAGACATGCCCTTTACAGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAAC
                                                                                                             AGCAGACATGCCCTTTACAGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAAC
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; 2000US-0250391P.
; 2000US-0251030P.
                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                8.9%;
                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                Score 238; DB 4;
Pred. No. 3.5e-78;
                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                  Length 354;
                                                                                                                                                                                                                                                                                                                                              Indels
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and

Gaps

364

110 304 0

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14-AUG-2000;

14-AUG-2000;

18-AUG-2000;

22-AUG-2000;

22-AUG-2000;

23-AUG-2000;

23-AUG-2000;

01-SEP-2000;

01-SEP-2000;

01-SEP-2000;

01-SEP-2000;

01-SEP-2000;

01-SEP-2000;

01-SEP-2000;

01-SEP-2000;

06-SEP-2000;

06-SEP-2000;

06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immunosuppressive; antiarthritic; 88; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; histomer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                 14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                    14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUN-2000;
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19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS26144 standard; cDNA; 354 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding a novel
2000US-0214886P

2000US-0211643P

2000US-021644P

2000US-0217496P

2000US-0217496P

2000US-022963P

2000US-0222964P

2000US-0225214P

2000US-0225214P

2000US-0225214P

2000US-0225266P

2000US-0225266P

2000US-02252679P

2000US-022575P

2000US-022934P

2000US-022934P
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2000US-0184664P.
2000US-0186350P.
2000US-0189874P.
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2000US-0198123P.
2000US-0205515P.
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                                                                                                                                                                                                                                                                                                                                                              cc rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used cin diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in calleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (RELISA). Disorders which are diagnosed or treated include autoimmune cd diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. carciac mepplasms of the breast or liver, cardiovascular disorders e.g. carciac carcest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by carciac, viruses and fungi and ocular disorders e.g. corneal infection, can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before can also be used to aid wound healing and epithelial cell proliferation, car segmenate tissues and in chemotaxis. The polypeptides can also be used cas a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, cased and ther nutritional components. The present for the present of the far the fat 
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488783/53.
P-PSDB; AAU16157.
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                                                                                                                                                                                                                                                                          238;
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                                            AGCAGACATGCCCTTTACAGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAAC
                                                                                                                                                                                         GCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGGTCAGG
                                                                                                                                                                                                                   GCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGGTCAGG
                                                                                                                                                                                                                                                                                                                                                          encodes a novel secreted protein of the data for this patent did not form part
                   AGCAGACATGCCCTTTACAGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barash SC,
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2000US-025198P.
2000US-0251479P.
2000US-0251856P.
2000US-0251868P.
2000US-0251869P.
2000US-0251989P.
2000US-0251989P.
2000US-0251989P.
2000US-0251989P.
2000US-0251989P.
2000US-0251989P.
                                                                                                                                                                                                                                                                          Conservative
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2000US-0249265P.
2000US-0249297P.
2000US-0249299P.
2000US-0249299P.
2000US-0250160P.
2000US-0250160P.
2000US-0250160P.
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                                                                                                                                                                                                                                                                                              Score 238;
Pred. No.
                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                            the printed
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assays

and

2000US-0240960P. 2000US-0241221P. 2000US-0241785P.

2000US-0241786P. 2000US-0241787P.

2000US-0249212P. 2000US-0249213P. 2000US-0249214P. 2000US-0249215P. 2000US-0249216P. 2000US-0249217P.

2000US-0246 2000US-0246 2000US-0246 2000US-0246 2000US-0246 2000US-0246 2000US-0246 2000US-0249 2000US-0249 2000US-0249 2000US-0249 2000US-0249 2000US-0249

46609P. 46610P. 46611P.

46613P. 49207P. 49208P.

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Gaps

0

424

364 110 304

170

2000US-024 2000US-024

2000US-024 2000US-024

4644617P. 466476P. 466477P. 466477P. 46523P. 46523P. 46520P. 465327P. 465327P.

2000US-0241808P. 2000US-0241809P. 2000US-0241826P.

2000US-024

2000US-024

08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
11-SEP-2000
11-SEP-2000
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11-SEP-2000
11-SEP-2000
11-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP

2000US-0237040P. 2000US-0239935P. 2000US-0239937P.

2000US-0237037P. 2000US-0237038P.

2000US-0236802P

2000US-0235836P. 2000US-0236327P. 2000US-0236368P. 2000US-0236368P. 2000US-0236369P. 2000US-0236370P.

2000US-0234274P. 2000US-0234997P. 2000US-0234998P.

2000US-0233065P. 2000US-0234223P.

2000US-0235484P. 2000US-0235834P.

2000US-0232398P. 2000US-0232399P. 2000US-0232401P. 2000US-0233401P. 2000US-0233063P. 2000US-0233064P.

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425

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RESULT 21
ABX73904
ID ABX73
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
22-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
haemostatic; antiarteriosclerotic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGAACACAACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAAGGCATGACACA 482
                                                  2000US-0216880P.
2000US-0217486P.
2000US-0217496P.
2000US-022964P.
2000US-022526P.
2000US-022526P.
2000US-022526P.
2000US-022526P.
2000US-0225427P.
2000US-0225479.
2000US-0225479.
2000US-0225479.
2000US-0226868.
2000US-0226868.
2000US-0226879.
2000US-0226879.
2000US-0226879.
2000US-0226879.
2000US-0236879.
2000US-02368029.
2000US-02368029.
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2000US-02368029.
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Human novel 18-MAR-2003 ABX73485 ABX73485

polymucleotide #313.

(first entry)

standard;

DNA;

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RESULT 22
ABX73485
ID ABX73
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AC ABX73
XX
DT 18-M2
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Best Local
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20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
17-NOV-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent human novel polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human novel polypeptides and their associated polymuclectides. The polypeptides and polymuclectides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus crythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointsstinal disorders, pulmonary disorders, cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders.
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RUBEN S M
BARASH S
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                                                                                                                                                                                       CGGAACACAACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGACACA 482
                                                                                                                                                                                                                                                     AGCAGACATGCCCTTTACAGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAAC 424
                                                                                                                                                                                                                                                                                                                   TGACACTGGAAGATACCAGCACCAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGA
                                                                                                                                                                                                                                                                                                                                                                                GCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGGTCAGG
                                                                                                                                                                                                                                                                                               TGACACTGGAAGATACCAGCACCAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGA
                                                                                                                                                                                                                                                                                                                                                           GCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGGTCAGG
                                                                                                                                                                         CGGAACACAACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGACACA
                                                                                                                                                                                                                                 AGCAGACATGCCCTTTACAGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAAC
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; 2000US-0241785P.
; 2000US-0241809P.
; 2000US-0244617P.
; 2000US-0249299P.
; 2000US-0251868P.
; 2000US-0251868P.
                                                                                                                                                                                                                                                                                                                                                                                                                      8.9%;
ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barash
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 238; DB o; L
; Pred. No. 3.5e-78;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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14 AUG-2000

14 AUG-2000

14 AUG-2000

14 AUG-2000

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14 AUG-2000

12 AUG-2000

30 AUG-2000

01 SEP-2000

01 SEP-2000

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02 SEP-2000

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29 SEP-2000

29 SEP-2000

20 CCT-2000

02 CCT-2000

03 CCT-2000

04 CCT-2000

05 CCT-2000

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01 CCT-2000

01 CCT-2000
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                            (ROSE/)
(RUBE/)
(BARA/)
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                            RUBEN S
BARASH
                                                                                       2000US-0225447P
2000US-0225758P
2000US-0225758P
2000US-0229343P
2000US-0229343P
2000US-0229343P
2000US-0229343P
2000US-0229343P
2000US-0233423P
2000US-023423P
2000US-023423P
2000US-023493P
2000US-023493P
2000US-023493P
2000US-023636P
2000US-023636P
2000US-023637P
2000US-0237039P
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2000US-0241785P
2000US-0241785P
2000US-0241869P
2000US-0251868P
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2000US-0225267P.
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2000US-0225270P.
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2000US-0220964P.
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2000US-0216847P.
2000US-0216880P.
2000US-0217487P.
2000US-0217496P.
2000US-0218290P.
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Matches 238;

Conservative

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3.5e-78

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Indels

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Gaps

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The invention relates to human novel polypeptides and their associated complynucleotides. The polypeptides and polynucleotides are useful in gene comply the treating, inhibiting or preventing neural disorders, immune comply for treating, inhibiting or preventing neural disorders, immune comply the disorders (e.g. systemic lupus exythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. cand multiple sclerosis), muscular disorders, respiratory diseases (e.g. cand multiple sclerosis), pulmonary disorders, reproductive disorders, completed disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left chart syndrome), renal disorders (e.g. acute kidney failure and end-stage crenal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and cappendicitis), allergic reactions and conditions (e.g. asthma), blood crelated disorders (e.g. thrombosis, atherosclerosis and myocardial cinfarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent comply the disease of the invention
                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular o renal disorders.
                                                                                                 Sequence 354 BP; 101 A; 79 C; 94 G; 77 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 323; 402pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-147444/14.
P-PSDB; ABU55225.
                       8.9%;
Score 238; DB; Pred. No. 3.50; Mismatches
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RESULT 23
ACH26450
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                                                                                                                                           Human; ss; sequencing by hybridisation; SBH; expressed sequence tag;
           30-JUL-2001; 2001US-00918995
                                   30-JUL-2001; 2001US-00918995.
                                                                                                                             genome mapping; biodiversity; genetic disorder
                                                                                                                                                                   Human adult ovary cDNA #4830.
                                                                                                                                                                                           13-OCT-2003
                                                                                                        Homo sapiens
                                                                                                                                                                                                                  ACH26450;
                                                                               US2003073623-A1
                                                                                                                                                                                                                                         ACH26450 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGGTCAGG
                                                                                                                                                                                                                                                                                                                                                                  AGCAGACATGCCCTTTACAGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAAC
                                                                                                                                                                                                                                                                                                                   CGGAACACAACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGACACA 482
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                                                                                                                                                                                                                                                                                                                                                    AGCAGACATGCCCTTTACAGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAAC
                                                                                                                                                                                                                                                                                                                                                                                                     TGACACTGGAAGATACCAGCACCAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                      TGACACTGGAAGATACCAGCACCAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGA 364
                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                         CDNA;
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Rosen

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Ruben SM,

Barash

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RESULT 24
ABA16633
ID ABA16
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AC ABA
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DT 23
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DB H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Sim
Matches 217;
               Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisckling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
                                                                                               Human nervous system related polynucleotide
                                                                                                                                                                                                ABA16633 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 449 BP; 147 A; 76 C; 86 G; 135 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide sequences obtained from as hybridization probes, as oligomers for F mapping, in the recombinant production of p
                                                                                                                                                                ABA16633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mapping, :
                                                                                                                                23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to 38043 CDNA Becharact
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(LABA/)
(STAC/)
(DICK/)
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LABAT I.
STACHE-CRAIN
DICKSON M C.
JONES L W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTTTCAAGGGAGAAGGGCAAGTTTATCAAAAACATTGTTTCAGGAGAAAGGGAGCATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 13662; 44pp; English.
                                                                                                                                                                                                                                                                                                      TAGCACAAATAATATAATTTATAATTTACAAATTGAC
                                                                                                                                                                                                                                                                                                                                                                        ATTTTTATTTTAATAGGTTTGGTGCTTATCTTCTAATAAGATTTAAATGTCACAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTACAGCCTACAGGACGTACACAATATCCTGCTGCTGGGAAAACCACAGCATTTTATCT
                                                                                                                                                                                                                                                                               TAGCACAAATAATATATTATAATTTACAAATTGAC
                                                                                                                                                                                                                                                                                                                                             ATTTTTTATTTAATAGGTTTGGTGCTTATCTTCTAATAAGATTTAAATGTCACAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTTTCAAGGGAGAAGGCAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA or RNA.
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                                                                                                                                (first entry)
                                                                                                                                                                                                DNA; 13836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1%;
100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m various cDNA libraries, useful
PCR, for chromosome and gene
protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
                                                                                               SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                           2661
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neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                           antiparasitic; cardiant; immune disorder; cardiovascular disorder;
         ds.
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16-AUG-2001

17-JAN-2001; 2001WO-US001334

2000US-0179065P. 2000US-0180628P. 2000US-0184664P. 2000US-0186350P.

16-MAR-2000; 17-MAR-2000; 18-APR-2000; 19-MAY-2000;

2000US-0198123P.
2000US-0209467P.
2000US-0214886P.
2000US-0216647P.
2000US-0216647P.
2000US-021664P.
2000US-0224518P.
2000US-0225214P.
2000US-0225214P.
2000US-0225214P.
2000US-0225266P.
2000US-0225266P.
2000US-0225447P.
2000US-0225447P.
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2000US-0225447P.
2000US-0225447P.
2000US-0225447P.
2000US-0225447P.
2000US-0225447P.
2000US-0231448P.
2000US-0231244P.
2000US-0231240P.
2000US-0231240P.
2000US-0233064P.
2000US-0233064P.
2000US-0233064P.
2000US-0234224P.

14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000

14-AUG-2000 12-AUG-2000 22-AUG-2000 22-AUG-2000 23-AUG-2000 30-AUG-2000 01-SEP-2000 01-SEP-2000 01-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 14-SEP-2000 14-SEP-2000

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17-NOV-2000
17-NOV-2000
17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
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08-DEC-2000
08-DEC-2000
                                            17-NOV-2000;
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                                                        L7-NOV-2000;
                                                                                                                     42221P.
44617P.
46474P.
46475P.
                                                                                             16528P.
                                                                                     6610P
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31-JAN-2000; 2000US-0179065P

17-JAN-2001; 2001WO-US001354.

09-AUG-2001. WO200157182-A2

domo sapiens.

Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.

Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3434.

06-NOV-2001

(first entry)

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RESULT 25
AAK58374
ID AAK58
XX AAK58
AC AAK58
AC
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Matches 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK58374 standard; cDNA; 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13836 BP; 3132 A; 3517 C; 3683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK58374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to (ABB14678-ABB18001) usefo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 8964; 1701pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-541565/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JAN-2001; 2001US-0259678P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 GGGTCTGGGGGTGGCATCTCCCCTAAAGGAAGTGGTCCCTCTGTGGCAAGTGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   709 GGGTCTGGGGGTGGCATCTCCCCTAAAGGAAGTGGTCCCTCTGTGGCAAGTGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCAGGATCAGGAGGATTTGGAGCCCCGTGAAGAAGAAATGAGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCAGGATCAGGAGGATTTGGAGCCCCGTGAAGAAGAAAATGAGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCTCCAGCTTTGCCTCAGCTCTCCCAGACAGAAAGACTGCGTCCTTTTCGTCGTTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCTCCAGCTTTGCCTCAGCTCTCCCAGACAGAAAGACTGCGTCCTTTTCGTCGTTCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.3%; Scc
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3224 human nervous system antigen polypeptides, diagnosing and/or treating nervous system cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel genes (ABA11004-ABA21534) and proteins ul for preventing, treating or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 169; DB
; Pred. No. 6.70
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G; 3504 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.7e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 13836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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FEB-2000 - MAR-2000 - MAR-2000 - MAR-2000 - MAR-2000 - MAY-2000 - MAY-2000 - MAY-2000 - JUN-2000 - JUN-

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2000US-018662P.
2000US-018635P.
2000US-018635P.
2000US-019813P.
2000US-019813P.
2000US-02014886P.
2000US-0214886P.
2000US-0214886P.
2000US-021688P.
2000US-021688P.
2000US-021829P.
2000US-021829P.
2000US-0225264P.
2000US-0225213P.
2000US-0231244P.
2000US-0231243P.
2000US-0231243P.
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2000US-0231243P.
2000US-0231244P.
2000US-0231243P.
2000US-0231242P.
2000US-0231242
02-OCT-2000

02-OCT-2000

13-OCT-2000

13-OCT-2000

20-OCT-2000

20-OCT-2000

20-OCT-2000

20-OCT-2000

20-OCT-2000

20-OCT-2000

08-NOV-2000

017-NOV-2000

117-NOV-2000

11
                     Nucleic acids encoding useful for preventing,
                                                                                         WPI; 2001-483426/52.
P-PSDB; AAM85593.
                                                                                                                                                                                                        (HUMA-)
                                                                                                                                                  CA,
                                                                                                                                                                                                             HUMAN
                                                                                                                                                           Barash
                                                                                                                                                                                                                                                2000US-0237038P.
2000US-0237039P.
2000US-0237049P.
2000US-0237049P.
2000US-0249960P.
2000US-0241809P.
2000US-0241809P.
2000US-0246471P.
2000US-0246471P.
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2000US-0246471P.
2000US-0246471P.
2000US-0246471P.
2000US-0246471P.
2000US-0246523P.
2000US-0246523P.
2000US-0246523P.
2000US-0246523P.
2000US-0246521P.
2000US-0246511P.
2000US-0246511P.
2000US-0249211P.
2000US-024921P.
2000US-0249211P.
2000US-025921P.
2000US-025921P.
2000US-025921P.
2000US-025921P.
2000US-025921P.
2000US-025921P.
2000US-025921P.
2000US-025929P.
200
                                                                                                                                                                                                           GENOME
                                                                                                                                                              SC,
                                                                                                                                                                                                           SCI
                       human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                              Ruben
                                                                                                                                                                                                           INC
                                                                                                                                                              MS
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26-JUL-2000
14-JUG-2000
12-JUG-2000
12-JUG-2000
13-JUG-2000
13-JUG-2000
10-SEP-2000
10-SEP-2000
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10-SEP-2000
10-SEP-2000
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10-SEP-2000
11-SEP-2000

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RESULT 26
ABN60913/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK34942 to AAK54950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytosca
gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For
                                                                                                                                                                                                                                                                                                                                    WO200214500-A2
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cancer related polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 825 BP; 216 A; 187 C; 206 G; 209 T; 0 U; 7 Other;
                                            Escobedo J, Garcia
Lamson G, Scott EM,
                                                                                                                                                                                                                                      16-AUG-2001; 2001WO-US025840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN60913 standard; cDNA; 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
WPI; 2002-241905/29
                                                                                                                                                                                       16-AUG-2000; 2000US-0226326P
                                                                                                                  (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1762 GACATCCTGAAGAATTACCTGGCAACCAGAGGTTTGACATGGAAAAAACATGTTGACCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1702 GAGCTCAACCTGGGTGACAAGTGTCTGGACGGCGTGCTGAACAACAACAACAGCTACGAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCGTTCTGT 1891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCTCGTGGCTCTCCAGCGGGAGTGTTTTCTGCTGTTTTACAGAGTCACGGGAGAC 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACATCCTGAAGAATTACCTGGCAACCAGAGGTTTGACATGGAAAAACATGTTGACCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCTCAACCTGGGTGACAAGTGTCTGGACGGCGTGCTGAACAACAACAGCTACGAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IJ
                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; tumour; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO 3434; 3071pp + Sequence Listing; English
                        a PD,
Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.2*;
99.5*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537
                                     Sudduth-Klinger J, Rein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 139; DB 4;
Pred. No. 1.3e-41;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                              gene mapping; tissue profiling;
ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO
                                                                  Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                               Labat
                                               H
                                                                     Randazzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467
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S 밁 S 밁 ঠ 밁 र्

New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

WPI; 2003-615964/58.

Claim

1; SEQ ID NO 2180; 44pp; English

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RESULT 27
ACH14968
ID ACH14
XX
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맑
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 78
                                                                                                                                                                                                                                                                                                                                                              Human;
genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polynucleotide (ABN27253-ABN33262) with cytostatic activity. The polynucleotide is used to produce a polypeptide, to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and to inhibit tumour growth. The polynucleotide is used as a probe in mapping and tissue profiling. The encoded polypeptide and antibodies to the polypeptide can also be used for therapeutic and diagnostic purposes. The polynucleotide is useful for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid for producing a polypeptide, detecting differentially expressed. genes correlated with a cancerous state of a mammalian cell, and inhibiting tumor growth.
                                                                                                                                                                                                                                                                                                            US2003073623-A1
                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                   Human adult brain cDNA #2180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                             Drmanac
                                                                                                                                                                             (LABA/)
(STAC/)
                                                                                                                                                                                                                                30-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                                          30-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                                                                    17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                              13-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACH14968 standard; cDNA; 476
                                                                                                                                                                                                        (DRMA/)
                                                                                                                                                                    (DICK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2026 AAAGCTCACCACGCCATG 2043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1966 CCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGGGGCCGTAACTGCCGCACTCAGGTG 2025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385
                                                                                                                                                                                                                                                                                                                                                           ss; sequencing by hybridisation; SBH; expressed sequence
mapping; biodiversity; genetic disorder.
                                                                                                                                                    LABAT I.
STACHE-CRAIN
DICKSON M C.
JONES L W.
                                                                                                                             RT,
                                                                                                                                                                                                       DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGGGCCGTAACTGCCGCACTCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGCTCACCACGCCATG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                           Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 181 A; 155 C; 159 G; 122 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID NO 880; 883pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.9%;
                                                                                                                                                                               B
                                                                                                                             Stache-Crain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.1e-19;
                                                                                                                             Dickson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 617;
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S
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RESULT 28
ABN33472
ID ABN33
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Best Local :
                                                                                                                                                                                                 New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit genome, useful for detecting tissue-, pathology-, and developmental-
The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple
                                                                                                                                                                                                                                                                                                                                                                             Shoshan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-2000; 2000US-0221607P
02-MAY-2001; 2001US-0287724P
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                                                                                                                  Example 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUL-2001; 2001WO-IB001903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human spliced transcript detection oligonucleotide SEQ ID NO:6220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN33472
                                                                                                                                                                         specific genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (COMP-) COMPUGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2046 ATTCAATCATATCTGTGAACAGACAAGGTTCAAAAACTAAGCATCCAGAGGCCCTGAGCA 2105
                                                                                                                                                                                                                                                                                                                         2002-257383/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse; rat; splice transcript; detection; RNA transcript;
variant; transcriptome; oligonucleotide library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77;
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                                                                                                                                                                                                                                                                                                                                                                                   Wasserman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                  ID NO 6220;
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                                                                                                               47pp; English.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
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                                                                                                                                                                                                                                                                                                                                                                             Faigler
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WPI; 1992-080075/10. P-PSDB; AAR21795.

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RESULT 29
AAQ22007/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC transcription units that populate a genome. The library comprises several CC oligonuclectides, each capable of hybridising selectively to a set of CC messenger RNAs transcribed from a given transcription unit of the genome, CC which encodes one or more messenger RNA splice variants. The CC oligonuclectide libraries are useful for detecting mRNAs from a CC biological sample, in expression profiling studies, in qualitatively or GC quantitatively characterising the corresponding transcriptome, and in CC detecting RNA transcripts and splice variants of human or animal CC transcriptomes. The libraries may also be used as specialised mini CC libraries to detect transcripts of a sub-transcriptome under a particular CC biological or pathological state, and so allowing the detection of tissue CC and pathology-specific genes such as those genes only expressed in Secific tissue under a specific pathological condition; to detect RNA transcripts and splice CC variants of a transcriptome of a patient suffering from a particular CC developmental specific genes; and to detect RNA transcripts and splice CC variants of a transcriptome of a patient suffering from a particular CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from CC part of the printed specification, but was obtained in electronic format CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity
Matches 60; Conserv
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25-MAR-2003
09-JUN-1992
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                                                        Breitenede
Kraft D, F
                                                                                                                                   08-AUG-1990;
11-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoding Cor a I allergen of hazel
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                                                                                                                                                                                                                                                                                                                                                                           Fagales.
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                                                                                                     (BIOM-) BIOMAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1843 GGAGTGTTTCTGCTGTCTGATTACAGAGTCACGGGAGACACCGTTCTGTGTTACTGCTGT 1902
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                                                        Rumpold H, Scheiner
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                                                                                                                                   90AT-00001668.
91US-00683831.
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846. .860
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                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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100.0%; Pr
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er O;
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3.4e-12;
                                                                        Hoffmannso
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                                                                        Breitenbac
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RESULT 30
ADF4559/c
ID ADF455,
XX ADF455,
XX ADF455,
XX ADF455
XX ATABID
DE Arabid
XX Promot
KW Altern
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Best Local
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The present invention describes a promoter (I) comprising DNA having any one of 21 1000-nucleotide long sequences (SI, see ADF45522), DNA having nucleotides in which one or more of nucleotides of (SI) is deleted, substituted or added and functions as disease stress-responsive promoter (DP), and DNA which hybridises with (SI) and functions as DP. Also described: (I) an expression vector (II) comprising (II); 2) a transformed organism (III) comprising (II); and (3) producing stress resistant plant by (III). (I) responds to disease stress, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The CDNA sequence encoding the Cor a I allergen of hazel was obtd. from the polyA+ mRNA isolated from ripe hazel pollen. The resulting CDNA was amplified by PCR using primers whose sequences were derived from the N-terminal amino-acid sequence of Cor a I. The DNA fragment produced was
                                                                                                                                                                                                                                                                                                                                                               Novel stress-responsive promoter useful for producing resistant plants, for elucidating disease stress resis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter; disease stress-responsive promoter; stress resistance; Alternaria brassicicola infection; infection;
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                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RIKA ) RIKAGAKU KENKYUSHO
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, useful in
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                                                                                                                                                                                                                                                                           SEQ
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                                                                                                                                                                                                                                                                     ID NO 18; 24pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54pp;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter SEQ ID NO:18.
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Query Match Best Local

Similarity

0.9%;

Score 25; Pred. No.

19 19

u •

Length 1085

Sequence

1085 BP;

208 A; 391 C; 330 G;

156 T; 0 U; 0 Other;

The present sequence encodes a chitinase polypeptide. The specification describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896, AAB18896, and AAB188902-05), and glucosyl hydrolase family 18 chitinases (AAB18895, AAB18897-98 and AAB18900-01). The level of chitinase in plar can be modulated to enhance disease resistance in crop plants and for control of pathogens. The chitinase polymucleotides are also useful as molecular markers for genotype in a plant, and for sequence shuffling

specification

plants

New maize chitinase genes encoding seven chitinases of glucosyl hydrolase family 19 are useful for enhancing disease resistance in crop plants by

Claim 1; Page 79-81; 96pp; English.

modulating

its expression

in plants.

Simmons CR,

Yalpani

2000-628269/60.

AAB18901

(PION-) PIONEER HI-BRED INT

INC

24-MAR-1999;

99US-0125915P.

09-MAR-2000; 2000WO-US006121

28-SEP-2000.

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ARASOLLT 31
ARA96229
ID ARA96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stress is caused by black sooty-mould microbe (Alternaria brassicicola) infection. (III) is useful for producing a transgenic plant. (I) is useful for producing a disease stress resistant plant and for elucidation the disease stress resistance response in plant. (I) enables the detection of stress caused by A. brassicicola infection. The present sequence represents an Arabidopsis thaliana disease stress-responsive promoter sequence, which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA96229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucosyl hydrolase family 19; glucosyl hydrolase famiy 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a maize chitinase polypeptide designated ZmChl3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "chitinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance; molecular marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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Pred. No.
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RESULT 32
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The invention relates to 63760 polypeptide (a human transporter family member, referred to as transporter-2 (TP-2)) and its corresponding nucleic acid. 63760 protein is useful for treating disorders characterised by insufficient or excessive production of a 63760 characterised by insufficient or excessive production of a 63760 compounds which modulate 63760 activity. 63760 DNA is used in gene therapy. 63760 protein, DNA and its antibody are useful for screening cassays, predictive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenetics); and methods of treatment (e.g., therapeutic and prophylactic). 63760 protein, DNA and its antibody are useful as a novel diagnostic target and therapeutic agent in assays applicable to treatment and diagnostic target and therapeutic agent in assays applicable to treatment and diagnosis of 63760 mediated or related disorders including central nervous system disorders such as atteriosclerosis, restenosis, myocardial infarction, etc; cancer by modulating cellular growth, differentiation or migration; hormonal disorders such as pituitary disorders (growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hormonal disorder; pituitary; thyroid; hyperthyroidism; hypothyroidism; immune; transient hypogammaglobulinaemia; immunestimulator; anorectic; congenital X-linked infantile hypogammaglobulinaemia; sugar homeostasis; anorexia; neuroprotective; antiarteriosclerotic; cardiant; cytostatic; antidepressant; vasotropic; anticonvulsant; nootropic; metabolic;
                                                                                                                                                                                                                                                                                                                                                                                                  Novel human transporter 2 polypeptide referred as 63760 polypeptide which is a member of human transporter family, useful as reagents or targets for treating TP-2 mediated disorders such as senile dementia, depression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Curtis RAJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; 63760 protein; transporter-2; TP-2; drug screening; gene therapy; pharmacogenetics; central nervous system; Alzheimer's disease; epilepsy; senile dementia; depression; cardiac related disorder; arteriosclerosis; restenosis; myocardial infarction; cancer; cell differentiation; growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human transporter-2 (TP-2) cDNA, 63760.
                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 1; 96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAE24349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-2000; 2000US-0233790P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1061 AATTGACAAAAAAAAAAAAAAAA 1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Human transporter-2 (TP-2) protein"
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RESULT 33
ADD37442
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Best Local S
Matches 25
                                                                                                                                                                                                                                                                         14-MAY-2001;
29-JUN-2001;
31-JUL-2001;
19-SEP-2001;
25-SEP-2001;
05-OCT-2001;
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05-OCT-2000;
14-NOV-2000;
15-NOV-2000;
15-DEC-2000;
18-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders), thyroid disorders (hyperthyroidism, hypothyroidism), etc; immune disorder such as transient hypogammaglobulinaemia, congenital X-linked, infantile hypogammaglobulinaemia, etc; disorders associated with sugar homeostasis such as obesity, anorexia, etc. The 63760 molecules are useful as surrogate markers for one or more disorders or disease states or for conditions leading up to disease states, as pharmacodyanamic markers and as pharmacogenomic markers. The present sequence is human TP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; gene; transporter; cytostatic; anorectic; antidiabetic; anticonvulsant; gene therapy; PGC-1 associated disorder; liver tum
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                                                                                                                                         Curtis RAJ,
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22-JAN-2001;
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                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC.
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                                                                       2003-851783/79.
DB; ADD37443.
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2001US-00957664.
2001US-00964295.
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2001US-0263169P.
2001US-00858194.
2001US-00895811.
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2000US-0238336P.
2000US-0248364P.
2000US-0248878P.
2000US-0256240P.
2000US-0256588P.
2000US-0256588P.
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2000US-0215376P.
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2002US-00055025
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2000US-0233790P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetes
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; Pred. No.
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17;
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New isolated nucleic acid, useful for preparing a composition for treating PGC-1 associated disorders e.g. liver tumors, obesity, e

obesity, epilepsy

diabetes

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RESULT 34
ABZ15532/c
ID ABZ155
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Best Local S
Matches 25
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The invention relates to identifying a stress condition to which a cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polymucleotides in the plant cell with array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polymucleotides in the plant cell characteristic of a stress response. The method is useful in the .
                                                                                                                                                                                                                                                                                                      24-AUG-2000; 2000US-0227866P
26-JAN-2001; 2001US-0264647P
22-JUN-2001; 2001US-0300111P
                                                                                                                                           Identifying a stress condition to which a plant cell has been exposed producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200216655-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis
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                                                                                                                                                                                             2002-304127/34.
                                                                                                               144;
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25; Conserv
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SYNGENTA PARTICIPATIONS
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                                                                                                               SEQ ID NO
                                                                                                                                                                                                                         Kreps J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thaliana;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thaliana stress regulated
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llarity 100.0%;
Conservative
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                                                                                                          3337; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                       Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stress;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3337.
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Query Match

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733 A; 326

269

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                                                                                                                                                                                                                                                                               Chang H,
Katagiri
                                The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is
                                                                                                                                                                                                      Identifying at least pathogenic infection bacterial, fungal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not represented in the printed sinformation supplied to Derwent
                                                                                                                                                                   Claim
                                                                                                                                                                                           gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant; bacterial infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
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                                                                                                                                                                27; SEQ ID NO 2374; 899pp; English
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                                                                                                                                                                                                                                                                                               Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thaliana gene,
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S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
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                                                                                                                                                                                                      one gene involved in plant resistance of conferring resistance or tolerance viral infection by determining or detection
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Pred. No.
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RESULT 37
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Matches 25
                                                                                                                                                                                                                                                                      synthetase (PAPSS) polynucleotide. A reduction of function pry-1 (axin) mutant in Caenorhabditis elegans was used to identify the T14G10.1 gene as a modifier of the AXIN pathway. Human orthologues, termed PAPSS, of this gene were then identified. These are attractive drug targets for the reatment of pathologies associated with a defective AXIN signalling pathway, such as cancer. In vitro and in vivo methods of assessing PAPSS function are provided. Modulation of the PAPSS or its binding partner can be used to examine the association of the PAPSS or its binding partner can be used to examine the association of the PAPSS another in mealthy and disease conditions and to develop diagnostic and therapeutic modalities for AXIN related pathologies. PAPSS-modulating agents that act by inhibiting or enhancing PAPSS expression, directly or indirectly, e.g. by affecting a PAPSS function such, can be identified using methods of the invention. Preferred modulating agents include antisense oligomers and phosphorothioate morpholino oligomers.
                ADA68659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a candidate AXIN pathway-modulating agent, useful in diagnosing and treating breast, colon, head and neck, kidney, lung, ovary, prostate or skin cancer, by providing an assay system comprising PAPSS polypeptide or nucleic acid.
                                              ADA68659 standard; DNA; 95769
                                                                                                                                                                                                                                             Sequence 2424 BP; 661 A; 565 C; 596 G; 602 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of a human phosphoadenosine-phosphosulfate synthetase (PAPSS) polynucleotide. A reduction of function pry-1 (axin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADK67852 standard; cDNA; 2424 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 8; 64pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphoadenosine-phosphosulfate synthetase, modifier of AXIN pathway.
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                                                                                                                        2394
                                                                                                                                        2655 AATTGACAAAAAAAAAAAAAAAAA 2679
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                                                                                                                                                                                     Similarity 25; Conserv
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                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                  Score 25; DB; Pred. No. 17; 0; Mismatches
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                                                                                                                        2418
                                                                                                                                                                                                  DB 12;
17;
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ABL86644
ID ABL86
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29-MAY-2001; 2001WO-US017756 26-MAY-2000; 2000US-0207484P Homo sapiens. WO200192581-A2 06-DEC-2001. Human; ovarian cancer; ovarian tumour;

cytostatic; gene;

88

ABL86644; 17-MAY-2002 Human ovarian

cancer related cDNA clone SEQ ID NO:9622.

(first entry)

ABL86644 standard; cDNA; 199

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                                                                                                                              Matches
                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                               The present invention relates to a method (MI) for identifying genes involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chang H,
Katagiri
                                                                                                                                                                                                                                                        Sequence 95769 BP; 30958 A; 16961 C; 16682 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 1979; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-175290/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-2001; 2001WO-IB001105
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5271 AATTGACAAAAAAAAAAAAAAA 5295
                                                         2655 ААТТGАСАЛАЛАЛАЛАЛАЛАЛАЛ 2679
                                                                                                                              25;
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F, Quan S,
                                                                                                                              Conservative
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S, Tao Y,
                                                                                                             0.9%; 5c.
100.0%; Pr/
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                                                                                                                                                            Score 25;
Pred. No.
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Whitham S, Xie
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9.4
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e Z, Zhu T,
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RESULT 39
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Best Local S
Matches 24
                                                                                                                                                                                                                                  Human; DNA-binding protein; histone; chromo domain protein; chromatin organisation modifier; Y-box binding protein; DNA organisation modifier; y-box binding protein; DNA organiser transcription; malignant disease; autoimmune disorder; rheumatic disease; genetic abnormality; infectious disease; neurological disorder; gene therapy; immunomodulatory; anti-HIV;
    31-JAN-2000; 2000US-0179065P.
04-FEB-2000; 2000US-0180628P.
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                                                                                                                                                                                                                                                                                                                                                             cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                    21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS29141 standard; cDNA; 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 199 BP;
                                                             17-JAN-2001; 2001WO-US001305
                                                                                                                                           WO200155162-A1.
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                                                                                                                                                                                sapiens
                                                                                                                                                                                                                     rheumatic;
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Similarity· 100.0%;
24; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                         for human DNA-binding protein #112.
                                                                                                                                                                                                                   sorder; gene therapy; immuno
anti microbial; cytostatic;
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Pred. No. 58;
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    14-AUG-2000

12-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

01-SEP-2000

02-SEP-2000

21-SEP-2000

21-SEP-2000

22-SEP-2000

23-SEP-2000

29-SEP-2000

29-SEP-2000

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02-SEP-2000
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28 - JUN - 2000

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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
2000US-0184664P.
2000US-0189874P.
2000US-0199076P.
2000US-0205515P.
2000US-0215135P.
2000US-0215135P.
2000US-0215135P.
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2000US-0215135P.
2000US-0215135P.
2000US-0216647P.
2000US-021748P.
2000US-021748P.
2000US-021748P.
2000US-022964P.
2000US-0225269P.
2000US-0225269P.
2000US-0225269P.
2000US-0225275P.
2000US-022575P.
2000US-022575P.
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2000US-022575P.
2000US-022575P.
2000US-022575P.
2000US-0231244P.
2000US-023348P.
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2000US-023333P.
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13-OCT-2000

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20-OC
             Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, Alzheimer's and Parkinson's diseases and cancers.
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17-NOV-2000;
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)B; AAU18265.
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2000US-0246532P

2000US-0246631P

2000US-0246611P

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2000US-0249210P

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2000US-02567198P.
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2000US-0251479P.
2000US-0251866P.
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2000US-0237040P.
2000US-0239935P.
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2000US-0254097P
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2000US-0246474P.
2000US-0246475P.
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2000US-0241826P.
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2000US-0246525P.
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2000US-0246523P.
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RESULT 40
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ID AAS29069
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Best Local Similarity
                                                           31-JAN-2000;

04-FEB-2000;

24-FEB-2000;

02-MAR-2000;

16-MAR-2000;

17-MAR-2000;

18-AFR-2000;

19-MAY-2000;

07-JUN-2000;

28-JUN-2000;

28-JUN-2000;

07-JUL-2000;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4;
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                               2000US-0179065P.
2000US-0184664P.
2000US-0186350P.
2000US-0186350P.
2000US-019874P.
2000US-0198123P.
2000US-0205515P.
2000US-0205467P.
2000US-0214886P.
2000US-0216847P.
2000US-0216847P.
2000US-0216847P.
2000US-0217486P.
2000US-0217487P.
2000US-0217486P.
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Pred. No.
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Nucleic acid mo
proteins, used
Alzheimer's and
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17-NOV-2000
17-NOV
The present invention relates to the isolation of novel DNA-binding proteins (AAU18194-AAU18281), and cDNA and genomic sequences encoding for these proteins. DNA-binding proteins such as histones, chromo (chromatin organisation modifier) domain proteins, and y-box binding proteins may contribute to disease resulting from aberrant DNA organisation and/or gene transcription. The sequences of the invention are useful in screening assays to identify antagonists and/or agonists that may enhance or block activities mediated by DNA-binding proteins. Blockers of DNA-binding proteins may be useful in treating disorders such as malignant diseases (e.g. cancer), autoimmune disorders (e.g. diabetes mellitus), rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-465557/50.
P-PSDB; AAU18193.
                                                                                                                                                                                                                                                         Claim
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2000US-0246525P.
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2000US-0246529P.
2000US-0246611P.
2000US-0246611P.
2000US-0249219P.
2000US-0249219P.
2000US-0249211P.
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2000US-02592186P.
2000US-0251868P.
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2000US-0251868P.
2000US-0251868P.
2000US-0251868P.
2000US-0251869P.
2000US-0251989P.
2000US-0251989P.
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disorder,
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26-JUL-2000;
14-AUG-2000;
12-AUG-2000;
12-AUG-2000;
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13-AUG-2000;
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15-SEP-2000;
16-SEP-2000;
17-SEP-2000;
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18-SEP-2000;
18-SEP-2000;
18-SEP-2000;
19-SEP-2000;
11-SEP-2000;
11-SE

2000US-022963P.
2000US-0224518P.
2000US-0224518P.
2000US-022526P.
2000US-022526P.
2000US-022526P.
2000US-0225270P.
2000US-0225758P.
2000US-0225759P.
2000US-0225758P.
2000US-0225758P.
2000US-023734P.
2000US-023943P.
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                                                                                                                         14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acute glomerulonephritis; cardiovascular disorder; respiratory disorder; Goodpasture's syndrome; neurological disorder; Alzheimer's disease; Parkinson's disease; endocrine disorder; Addison's disease; gene; reproductive system disorder; endometriosis; infectious disease; viral infection; bacterial infection; fungal infection; vaccine; gastrointestinal disorder; multiple sclerosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; DNA-binding protein; B cell immunodeficiency; autoimmune disorder; severe combined immunodeficiency; rheumatoid arthritis; Crohn's disease; diabetes mellitus; allergy; asthma; inflammatory condition; thrombosis; graft-versus-host disease; blood-related disorder; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                           17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding human
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                      2000US-0216647P
2000US-0216880P
2000US-021748FP
2000US-021748FP
2000US-022964P
2000US-022964P
2000US-0224518P
2000US-0224518P
2000US-022568P
2000US-022568P
2000US-0255757P
2000US-0255757P
2000US-025575PP
2000US-0257588P
2000US-0225758PP
2000US-022584PP
2000US-0229344PP
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Pred. No.
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Matches Query Match

Local

Similarity

0.9%;

Score 24; Pred. No.

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Length 222;

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05-SEP-2000

08-SEP-2000

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21-SEP-2000

25-SEP-2000

27-SEP-2000

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29-SEP-2000

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20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
17-NOV-2000;
                                                                                                                                                                immunodeficiencies (e.g. B cell immunodeficiencies, severe combined immunodeficiencies), autoimmune disorders (rheumatoid arthritis, multiple sclerosis, diabetes mellitus), allergic reactions and conditions (e.g. asthma), inflammatory conditions, graft-versus-host disease, blood-related disorders (thrombosis, atherosclerosis), hyperproliferative disorders (e.g. cancer), renal disorders (e.g. acute glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders (Goodpasture's syndrome), neurological disorders (e.g. Addison's disease), reproductive system disorders (e.g. endometriosis), infectious disease), reproductive system disorders (e.g. endometriosis), infectious
                                         useful to stimulate neuronal growth and treat, prevent, and/or diagnose neuronal damage which occurs in certain neuronal disorders or neuro-degenerative conditions. The present nucleic acid sequence encodes a human DNA-binding protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                     disease), reproductive system disorders (e.g. endometriosis), infectious diseases (e.g. viral, bacterial or fungal infections) and gastrointestinal disorders (e.g. Crohn's disease). The invention is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ROSE/)
(RUBE/)
(BARA/)
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                Novel DNA-binding protein useful for diagnosis, prognosis, prevention treatment of immune, hyperproliferative, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen
                            http.seqdata.uspto.gov/sequence
                                                                                                                                                                                                                                                                                                                                      The present invention relates to a new DNA-binding protein. The invention
                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
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RUBEN
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222
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2000US-0237033P.
2000US-0237039P.
2000US-0239939P.
2000US-0240960P.
2000US-0241785P.
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2000US-0234274P.
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, endocrine, gastrointestinal
BP; 112 A; 26 C; 25
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Other;
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and

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RESULT 42
ABS68209
ID ABS68
14-AUG-2000

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14-AUG-2000

14-AUG-2000

12-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000

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02-SEP-2000

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02-OCT-2000

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02-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reproductive system disorder; endometriosis; infectious disease; viral infection; bacterial infection; fungal infection; vaccine; gastrointestinal disorder; multiple sclerosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyperproliferative disorder; cancer; renal disorder; arrhythmia; acute glomerulonephritis; cardiovascular disorder; respiratory disorder; Goodpasture's syndrome; neurological disorder; Alzheimer's disease; Parkinson's disease; endocrine disorder; Addison's disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetes mellitus; allergy; asthma; inflammatory condition; thrombosis;
graft-versus-host disease; blood-related disorder; atherosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding protein; B cell immunodeficiency; autoimmune disorder; combined immunodeficiency; rheumatoid arthritis; Crohn's disease;
                                 2000US-0229343P
2000US-0229343P
2000US-0229345P
2000US-0229509P
2000US-0231413P
2000US-0231413P
2000US-0234274P
2000US-0234274P
2000US-0234274P
2000US-0234274P
2000US-0236327P
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2000US-0236370P
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2000US-0225757P.
2000US-0225758P.
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2000US-0217487P.
2000US-0217496P.
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2000US-0228924P.
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2000US-0220963P.
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RESULT 43
ADC25203
ID ADC25
XX ADC25
XX ADC25
XX IB-DE
XX IB-DE
XX Humar
XX Extra
KW neurc
KW neurc
KW cardi
KW rooti
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                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a new DNA-binding protein. The invention CC is useful in treating, preventing, diagnosing and/or prognosing CC immunodeficiencies (e.g. B cell immunodeficiencies) severe combined immunodeficiencies), autoimmune disorders (theumatoid arthritis, multiple CC sclerosis, diabetes mellitus), allergic reactions and conditions (e.g. CC asthma), inflammatory conditions, graft-versus-host disease, blood-related disorders (thrombosis, atherosclerosis), hyperproliferative conditions (e.g. cancer), renal disorders (e.g. acute glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders (c.g. ardiovascular disorders (e.g. arrhythmia), respiratory disorders (c.g. disease, Parkinson's disease), endocrine disorders (e.g. Alzheimer's CC disease, Parkinson's disease), endocrine disorders (e.g. Alzheimer's CC disease, reproductive system disorders (e.g. endometriosis), infectious CC disease, viral, bacterial or fungal infections) and CC disease (e.g. viral, bacterial or fungal infections) and CC disease (e.g. viral, bacterial or fungal infections) and CC disease (e.g. viral, bacterial or fungal infections and/or diagnose CC degenerative conditions. The present nucleic acid sequence encodes a continual protein of the invention. Note: The sequence encodes a continual protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was contained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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20-OCT-2000;
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08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel DNA-binding protein useful for diagnosis, prognosis, prevention treatment of immune, hyperproliferative, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.
                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ROSE/)
(RUBE/)
(BARA/)
 nootropic; antia
neural disorder;
                                 respiratory-Gen; immunosuppressive;
                                               cardiovascular-Gen;
                                                                             Extracellular matrix protein;
                                                                                                                                              18-DEC-2003
                                                                                                                                                                          ADC25203;
                                                                                                                                                                                                         ADC25203
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                                                                neuroprotective;
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BARASH
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                antiallergic;
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; 2000US-0241785P.
; 2000US-0241809P.
; 2000US-0244617P.
; 2000US-0249299P.
; 2000US-0251868P.
; 2000US-0251868P.
                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                             extracellular matrix gene
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                                            trix protein; cytostatic; antibacterial; virucide;
gynaecological; gastrointestinal-Gen; cardiant;
en; nephrotropic; antiinflammatory; muscular-Gen;
                                                                                                                                                                                                         CDNA;
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                  cancer; bacterial
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                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                  cerebroprotective;
cterial infection; v
                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                  T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                    Length 222;
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                  viral
                  infection;
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32397P 32398P 32399P 32400P 32401P 33064P	1414P 12080P 2081P 1968P	1243P	0437P 0438P	9509P	9344P	9287P	7009P	6868P	62795	5758P	5447P 5757P	5268P	25266P	25213P 25214P	24518P 24519P	20963P 20964P	17496P	17487P	16647P	L4886P)5515P)9467P	98123P	9874	36	0628		101403				7	rdiova
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05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000;	EC-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	OV-2000;	CT-2000;	CT-2000;	CT-2000;	CT-2000;	CT-2000;	CT-2000;	CT-2000;	CT-2000;	CT-2000;	EP-2000;	EP-2000;	EP-2000;	SEP-2000;	EP-2000;	EP-2000;
2000US- 2000US- 2000US- 2000US- 2000US- 2000US- 2000US- 2000US-	2000C	20000	20000	20000	20000	20000	20000	20000	2000	20000	20001	20001	20000	20000	20000	20001	20001	20001	20000	20000	20000	20001	20000	20001	20000	20000	2000	20001	20001	20001	2000	2000
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-0251030 -0251988 -0256719 -0251479 -0251856 -0251868	0000 0000 7000 7000	224	122	24	24	1	224	141	442	2 2	22	22	224	22	22	22	22	22	22	201	20	24	23	3 13	23	2 4	3 (2)	2 13	22 2	N	3 (2) (3 1.

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RESULT 44
ADC25275
ID ADC25275
AC ADC25
XX ADC25
XX ADC25
DT 18-DE
XX Humar
XX Extra
KW neurc
KW respi
KW respi
KW neurc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 24
                                                                                    Extracellular matrix protein; cytostatic; antibacterial; virucide; neuroprotective; gymaecological; gastrointestinal-Gen; cardiant; cardiovascular-Gen; nephrotropic; antiinflammatory; muscular-Gen; respiratory-Gen; inmunosuppressive; cerebroprotective; vasotropic; nootropic; antiallergic; cancer; bacterial infection; viral infection; neural disorder; immune system disorder; plood disorder; neurodisorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; pulmonary disorder; proliferative disorder; human; gene therapy; ss. gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA-binding proteins and gene encoding them, useful for diagnosing, treating and/or preventing e.g. neurological, inflammatory, infectious, cardiovascular, autoimmune, respiratory, neoplastic or digestive diseases.
                                                                                                                                                                                                                                                                                                                                          Human cDNA from extracellular matrix gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC25275 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2003
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P-PSDB; ADC25331.
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11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
17-JAN-2001; 2001US-00764846.
                            Homo sapiens
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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57;
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24-FEB-2000)
24-FEB-2000)
24-FEB-2000)
12-MAR-2000)
11-MAR-2000)
11-MAR-2000)
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CC (expressing the protein), the extracellular matrix proteins (including CC their fragments, epitopes and homologues), an isolated antibody that CC binds specifically to the protein, diagnosing a pathological condition or Susceptibility to a pathological condition (comprising determining the presence or absence of the mutation), diagnosing a CC condition based on the presence or absence of the mutation), diagnosing a CC pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition of the CC pathological condition or susceptibility to a pathological condition of CC comprising determining the presence or amount of expression of the CC protein in a biological sample and diagnosing a condition based on the CC protein to a mammalian subject, identifying a binding partner to the protein, the gene corresponding to the CDNA sequence, and identifying an activity in a biological assay (comprising expressing the nucleic acid in a seal, isolating the supernatant, detecting an activity in a biological assay in the supernatant having the call activities Cytostatic, antibacterial, Virucide, Neuroprotective,
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA-binding proteins and gene encoding them, useful for diagnosing, treating and/or preventing e.g. neurological, inflammatory, infectious, cardiovascular, autoimmune, respiratory, neoplastic or digestive
                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (cDNA) encoding a human extracellular matrix protein, representing one convel genes. Also included are recombinant vectors, host cells
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RESULT 45 ABV20036 Human prostate expression marker cDNA 20027 ABV20036; ABV20036 13-SEP-2002 (first entry) standard; cDNA; 291 BP

Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.

20-FEB-2001; WO200160860-A2 Homo sapiens. 2001WO-US005171

17-FEB-2000; 16-MAR-2000; 25-MAY-2000; 09-JUN-2000; 18-JUL-2000; 13-DEC-2000; ; 2000US-0183319P. ; 2000US-0189862P. 2000US-0207454P. ; 2000US-0211314P. ; 2000US-0219007P. ; 2000US-0255281P.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE

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RESULT 46
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                                                  presence of prostate cancer, stage of prostate cancer.
                                                                         nucleic acid molecule associated with cancerous state and correlating with presence of prostate cancer, use
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Claim

1; Page 9711; 11750pp; English

The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding the a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as superseed sequence tags (EST) for inforensics, in assessing biodiversities, or in identifying mutations

was ť

of.

New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

Claim 1; SEQ ID NO 10672; 44pp; English.

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ACH23460
ID ACH23
XX Human
XX 
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genome
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mapping; biodiversity; genetic disorder.
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JONES L W.
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RESULT 48
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (II) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 11581; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-2000;
16-MAR-2000;
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                The invention relates to 50 novel ESTs (expressed sequence tags; ACC60450 ACC60499) obtained from a rice leaf cDNA library. The invention also relates to a biochip comprising these ESTs. The biochip of the invention can be used in a variety of agricultural applications. It can be used in the cloning of genes which confer useful characteristics in crop species, to predict hybrid vigour (heterosis) at an early stage, in the detection of transgenic agricultural produce, in screening for novel herbicides and pesticides and in disease diagnosis. The biochip may also be used in medical research. The present sequence represents a rice leaf EST of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice leaf EST; expressed sequence tag; biochip; DNA array; cloning; detection; heterosis; hybrid vigour; transgene detection; herbicide screening; disease diagnosis; medical research; agriculture; ss.
                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 23 (Disclosure); 29pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice leaf expression sequence labels and constituted biochip
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                                                                                                                                                                  The invention relates to 50 novel ESTs (expressed sequence tags; ACF56894 -ACF56943) obtained from a rice leaf cDNA library. The invention also relates to a biochip comprising these ESTs. The biochip of the invention can be used in a variety of agricultural applications. It can be used in the cloning of genes which confer useful characteristics in crop species, to predict hybrid vigour (heterosis) at an early stage, in the detection of transgenic agricultural produce, in screening for novel herbicides and pesticides and in disease diagnosis. The biochip may also be used to assess the safety of transgenic agricultural products. The present sequence represents a rice leaf EST of the invention
                                                                                                                                    Sequence 532 BP; 140 A; 108 C; 118 G; 166 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 23 (Disclosure); Opp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                               Rice leaf specific expression sequence label and its biochip prepared
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sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp434N2420) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp434N2420 Further information about the clone and the sequencing project is Location/Qualifiers 1.2297 /organism="Homo sapiens" /mol type="mgNNA" /db_xref="RZPD:DKFZp434N2420" /db_xref="RZPD:DKFZp434N2420" /tissue type="testis" /clone="DKFZp434N2420" /tissue type="testis" /clone="DKFZp434N2420" /db_sref="spen:DKFZp434N2420" /tissue type="testis" /clone="DKFZp434N2420" /db_sref="spen:DKFZp434N2420" /db_sref="spen:DKFZp434N2420" /tissue type="testis" /clone="DKFZp434N2420" /db_sref="spen:DKFZp434N2420" /db_sre	clum) MIPS, Ingolstaedter Landstr.1, D-8; Molecular Genome Analysis, German C . Email s wiemann@dkfz-heidelberg.de	Craniata; Vertebrata Catarrhini; Hominida Deutschenbaur,S., St Osanger,A., Fobo,G.,	mRNA 1 2420 (from				
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AL539798 Homo sapiens FE7
CSODF031YA23 5-PRIME, mRR
AL539798
AL539798.3 GI:45715436
EST.
Homo sapiens (human)
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31264361.
Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 990)
                                                                                                               Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                  GATTTAAATGTCACAAACTGTAGCACAAATAATATATATTATAATTTACAAATTGAC
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o sapiens FETAL BRAIN Homo sapiens
5-PRIME, mRNA sequence
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                  GGTGGCATCTCCCCTAAAGGAAGTGGTCCCTCTGTGGCAAGTGATGAAGTCTCCAGCTTT
                                                                                   TCTTCCACGGAGCCTTCTCCTGCAGGGCGAGAGCGTTCCTCCAGTTGTGGGGTCTGGGGGGT
                                                                                                                             TGCTTTGAGGAACCACAGCCATCAACATCGACGTCAGACCTCTTCCCCACAGCCTCGGCC
                                                                                                                                           TGCTTTGAGGAACCACAGCCATCAACATCGACGTCAGACCTCTTCCCCACAGCCTCGGCC
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619 660 559 499 540 439 480 379 420

900

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was not normalized. Library was constructed by Life Techno division of Invitrogen. This sequence belongs to sequence cluster 6792.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODF031AA12QP1&c=6792.
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                GTTCGGCGCGGGGGGGGGGGTGTAATCCCGATGGAGCGGCCCGAGGAAGAAGCAGTCG
                       CCCAGCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAAATCAGGT
                                                                                                                              GTCCTCCTGAGGAAGCGGGAGTGGACCATCGGGCGGAGACGAGGTTGCGACCTTTCCTTC
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ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol type="mrNA"
/db xref="taxon:9606"
/clone="CSODF031YA23"
/tissue_type="FETAL BRAIN"
/dev stage="fetal"
/clone lib="Homo sapiens FETAL BRAIN"
/clone lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotL-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 921)
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AGENCOURT 7940317 NIH MGC_67 Homo
5', mRNA sequence.
BU176559
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM13467 row: e column: 18
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                                                                                                                                                                                                                                                                                           TGTGTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGCAGAACA 1948
GAGCGTGTTTTTAAAATACAGAGACAAGCACGTCAAGGTGTTTTTCACAGCCCCCTGAGGG 2188
                                                                                                                                                   ACTGCCGCACTCAGGTGAAAGCTCACCACCACGAAATTCAATCATATCTGTGAACAGA 2068
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                                                                                            CAAGGTTCAAAAACTAAGCATCCAGAGGCCCTGAGCAGCTTTCAGCACTGGAGGTGAAGA 2128
                                                                                                                             ACTGCCGCACTCAGGTGAAAGCTCACCACGCCATGAAATTCAATCATATCTGTGAACAGA
                                                                                                                                                                                                                                                                       TGTGTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGCAGAACA
                                                                                                                                                                                                 TTCCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGGGCCGTA
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIH_MGC_67"
/note="Organ: eye, Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon.9606"
/clone="IMAGE:6143609"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
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Catarrhini; Hominidae;
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RESULT 4
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AGENCOURT 7052199 NIH MGC_101 Homo
5', mRNA sequence.
BQ073354
                                                                                                                                                                                                                                        cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 992)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, N
                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                      High quality sequence stop: 670.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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/tissue_type="epidermoid carcinoma, cell line"
/lab host="DH10B (phage resistant)"
/clone_lib="NIH_MGC_101"
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5806143"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalian Gene Collection (MGC)
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RESULT 5
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Best Local Similarity
Matches 703; Conserv
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                                                       CD243458
AGENCOURT 14121909 N
IMAGE:30383176 5', m
CD243458
CD243458.1 GI:31003
EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                            Homo sapiens
                                         Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  into EccRI/KhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CNNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                      GI:31003922
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Tlssue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: NDAM446 row: j column: 17
High quality sequence stop: 660.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
NAtional Institutes of Health, Mammalian Gene Collection Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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GACAAGGTTCAAAAACTAAGCATCCAGAGGCCCTGAGCAGCTTTCAGCACTGGAGGTGAA
                                                                               TAACTGCCGCACTCAGGTGAAAGCTCACCACGCCATGAAATTCAATCATATCTGTGAACA
                                                                                                                   TAACTGCCGCACTCAGGTGAAAGCTCACCACGCCATGAAATTCAATCATATCTGTGAACA
                                                                                                                                                                             CATTCCTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGGGCCG
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/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:30383176"
/lab host="DH10B-Ton A ( T1 and T5 phage resistances)"
/clone="1b="NIH MGC_180"
/clone-"Organ: Testis, Vector: pCMV-SPORT6.1; Site 1: Not!
/note="Organ: Testis, Vector: pCMV-SPORT6.1; Site 1: Not!
Site_2: BcoRV (destroyed); Library is oligo-dT prImed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.68 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 2412)
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2 (bases 1 to 2412)
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CTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGGGCCGTAACT
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/db_xref="taxon:9606"
/clone="CSODFO17YI19"
/tissus_type="Fetal brain"
/plasmid="pCMVSPORT_6"
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1 (bases 1 to 897)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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602240332F1 NIH_MGC_46 Homo sapiens
     found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLCM1189 row: p column: 08
                                                                                                                         Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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                                                         CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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Location/Qualifiers
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Transcriptome characterization elucidates signaling net control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
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Insert Length: 755 Std Error:
Location/Qualifiers
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Fax: 650 473 7760
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230 Constitution Drive, Menlo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 755)
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High quality sequence stop: 775.
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1 (bases 1 to 840)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                       /clone="IMAGE:4580633"
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adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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EST.
                                                                                                                 Email: genomics@hri.co.jp
HRI human cDNA project; 5.- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
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1534 CACGCCCTGTGCACCTGCTTCCAGCCCATGCCCGACCGGAGAGCGGAGCGCGAGCAG 1593
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Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarzu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Sequencing by: Agencourt Hissocience Corporation
DNA Sequencing by: Agencourt Hissocience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                    BQ215731 870
AGENCORT 7549119 NIH_MGC_68
5', mENA Bequence.
BQ215731
BQ215731 GI:20397131
                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                Unpublished (1999)
                                                                                                                                                                                Homo sapiens
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/clone_lib="PLACE1"
/note="Vector: pME18SFL
                                                                                                                                                                                              (human)
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sapiens cDNA clone
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MAGE:6059147
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916 bl

AGENCOURT_6418058 NIH_MGC_71 Hc

5', mENA sequence.

BM459647

BM459647.1 GI:18508687

EST.

HOmo sapiens (human)
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Query Match
Best Local Similarity
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http://image.llnl.gov
plate: LLAM13325 row: f column: 12
High quality sequence stop: 601.
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            GCCCTGGGGGATGCACCCTCCACGTCCGCTCAGCCTGACGACAG 1498
                                                                                      AGGCAGGCGGCGCAGCCTCCCCCACTGCCCAGCACCCGAGGGGCGAGGCGAGCCAGGAGCCCCACAG 1455
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                                                                                                                                                         AGTGAGTCCTCAGACATTAGCCAGCCATACGTCGTGTGCCGGCAGTGTCCTGAGTACAGA 1395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="large cell carcinoma"
/lab how="DH10M (phage-resistant)"
/clone_lib="NIH_MGC_6"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo c
Average insert size 1.8 kb. Library constructed by Li
Technologies. "
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6059147"
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Бр Homo

sapiens

linear | cDNA clone

EST 05-FEB-2002 MAGE:5534277

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TITLE
JOURNAL
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Best Local :
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 916)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information ca
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12220 row: h column: 22
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Tissue Procurement: ATCC
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                                                                                                                                                                                                       GCTTGCTACTCGGGCTGGATGGAGCGCTCGTCCCTGTGTCCCTACCTGCCGCTGTCCCGTG 1128
                                                                                                                                                                                                                                                                                   GACGTCAGAGCAGCGGCTGGGAÁGCCAGACAAGATGGAGGÁGACGCTGACATGCATCATC
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                                                                      CCAGACAAGAGTCGCAGTGAAGAAGATGTGCAAAGTATGGATGCCAGGAATAAAATCACT
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/db_xref="taxon:9606"
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/clome_lib="NIH MGC_71"
/clome_tib="NIH MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_Site_2: SalI; Cloned unidirectionally. Primer:
Average insert size 2.1 kb. "
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/mol_type="mRNA"
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JOURNAL COMMENT
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Best Local Similarity
Matches 563; Conserv
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12185 row: k column: 22
High quality sequence stop: 666.
Location/Qualifiers
1. .1143
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1 (bases 1 to 1143)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1143 bp mRNA linear EST 20-FEB-200: AGENCOURT 6426028 NIH MGC_71 Homo sapiens cDNA clone IMAGE:5520909 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM542545.1 GI:18772149
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   ACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAGTTTCAAGGGAGA 2458
                                                                   GACGAAGCCTTTCTGTAACATGCGGCCGTCCCGCCGAGAGGGGCAGTTTTTGCTCTTTTTGT
                                                                                                                                      GGCCGCAGCCCGCCCTCCTGGTGAGCGCTGGGCAGGGCTCGTGGTGGCATCAGCAGCAGA
                                                                                                                                                                                                                                                                                          CTGAGCAGCTTTCAGCACTGGAGGTGAAGAGAGCGTGTTTTTAAAATACAGAGACAAGCA
                                                                                                                                                                                              CGTCAAGGTGTTTTCACAGCCCCCTGAGGGAAGGGACGCAGGGTCTCCGACAGGTGCTCT
                                                                                                                                                                                                                                                                                                                                            CTGAGCAGCTTTCAGCACTGGAGGTGAAGAGAGCGTGTTTTTAAAATACAGAGACAAGCA
                                                                                                                   GGCCGCAGCCCGCCTCCTGGTGAGCGCTGGGCAGGGCTCGTGGTGGCATCAGCAGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5520909"
/tissue_type="leiomyosarcoma"
/lab host="DHIOB (phage-resistant)"
/clone_lib="NIH_MGC_71"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                               21.0%; Score 563; DB 4; Lo
100.0%; Pred. No. 1.7e-269;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1143;
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Query Match 20.9%; Score 560; DB 2; Length 666; Best Local Similarity 99.8%; Pred. No. 5.2e-268; Matches 610; Conservative 0; Mismatches 1; Indels 0; Gaps Oy 1156 AACAACCTCGTGGAAGCATACCTCATCCAGCATCCAGACAAGAGTCGCAGTGAAGAAGAT Db 1 AACAACCTCGTGGAAGCATACCTCATCCAGCATCCAGACAAGAGTCGCAGTGAAGAAGAT Oy 1216 GTGCAAAGTATGGATGCCAGGAATAAAATCACTCAAGACATGCTGCAGCCCAAAGTCAGG Oy 1216 GTGCAAAGTATGGATGCCAGGAATAAAATCACTCAAGACATGCTGCAGCCCAAAGTCAGG OG 61 GTGCAAAGTATGGATGCCAGGAATAAAATCACTCAAGACATGCTGCAGCCCCAAAGTCAGG Db 61 GTGCAAAGTATGGATGCCAGGAATAAAATCACTCAAGACATGCTGCAGCCCCAAAGTCAGG OG 10 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM316 row: J column: 19 High quality sequence stop: 640. FEATURES Location/Qualifiers 1. 666 /organisms="Homo sapiens" /db xref="taxon:9606" /clone="IMAGE:3629682" /tissue_type="choriocarcinoma" /tissue_type="Thoriocarcinoma" /lab_hoSt="DH10B (phage-resistant)" /clone_lib="NHH MGC 21" /clone_lib="NHH MGC 21" /clone_lib="NHH MGC 21" /clone_lib="NHH MGC 21" /clone_lib="CoRI; cDNA made by oligo-dT priming. Directionally cloned into EccRI/XhoI sites using the following 5 adaptor: GGCRGAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."	HEGUTT 14 BE407732 BE407732 BE407732 BE407732 BE407732 BE407732 ACCESSION ACCESSION BE407732 VERSION BE407732 BE407732 BE407732 BE407732 GET. BE407732 BE407732	Qy 2459 AGGGCAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAGTTTACAGCCTACAG Db 397 AGGGCAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAGTTTACAGCCTACAG Qy 2519 GACGTACACAATATCCTGCTGCTGGGAAAACCACCACCAGCATTTTATCTTATTTTAATTTAA Db 457 GACGTACACAATATCCTGCTGCTGGGAAAACCACCAGCATTTTATCTATTTTATTTTAA Qy 2579 TAGGTTTGGTGCTTATCTTAATAAAACCACAAACTGTAGCACAAATAATA Db 517 TAGGTTTGGTGCTTATCTTCTAATAAGATTTAAATGTCACAAACTGTAGCACAAATAATA Db 517 TAGGTTTGGTGCTTATCTTCTAATAAGATTTAAATGTCACAAACTGTAGCACAAATAATA Db 517 TAGTTTATAATTTACAAATTGAC 2661 Db 577 TAATTTATAATTTACAAATTGAC 599
0; 1215 FEATURES 60 SOURCE 1275	RESULT 15 AL539797/c LOCUS DEFINITION ACCESSION VERSION VERSION VERSION REFERENCE SOURCE ORGANISM REFERENCE AUTHORS TITLE TOURNAL COMMENT P	Qy 1516	2518 Qy 1 456 Db 2578 Qy 1 516 Db 5638 Qy 1 576 Db 676 Db 676 Db
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6792.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODFO31AA12NP1&c=6792.r. Location/Qualifiers 11118 //organisms="Homo sapiens" //mol_type="mRNA" //db_xref="taxon:9606" //clone="CSODFO31YA23"	AL539797 AL539797 Homo sapiens FETAL BRAIN Homo sapiens CDNA clone CSODF031YA23 3-FRIME, mRNA sequence. AL539797 AL539797 AL539797.3 GI:45715435 EST. HOmo sapiens (human) Homo sapiens (chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1118) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) On Feb 15, 2001 this sequence version replaced gi:31264360. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned	TITTGTGAGCTACCTGGGGCTGCTGGTGCTGACCACGCCCGACCGGCTGGTGCTCAGCCCAGCCCAGCCCGACCGGCTGGTGCTCAGCCCAGCCCAGCCCGACCGGCTGTGCTCCAGCCCAGCCCAGCCCGACCGGCTGTGCTCCAGCCCAGCCCATGCCCGACCGGGACCCGGCTGCTGCAGCCCAGCCCAGCCCAGCCCGACCCGGGACCCGGCTGCAGCAGTGTGCGGGTCTGCCTGC	CGGTCTTTTTCTGATGAAGAAGGGAGTTCAGAGGACCTGCTGGAGCTGTCAGACGTTGAC

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RESULT 16
BF971838
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                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BF971838
                                                                                                                                                                                                                                                                                                                                                                  602240424F1 NIH_MGC_46 Homo
                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                              Homo sapiens
Homo sapiens
                                                                                                                                                                                                                                                                                                           BF971838.1 GI:12339053
                                                                                                                      Unpublished (1999)
            cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
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                                                                                                                                                                                     (bases 1 to 934)
Sequencing by: Incyte Genomics, Inc.
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/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNV
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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Pred. No. 1.7e-257;
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                                                                                                                                                                                                                                                                                                                                                                  4 bp mRNA linear EST 22-JAN-2001 sapiens cDNA clone IMAGE:4329076 5',
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Catarrhini; Hominidae;
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639; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGCAGAACATTCCTGCTTCCGAGTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCAGAGGCCCTGAGCAGCTTTCAGCACTGGAGGTGAAGAGAGCGTGTTTTTAAAATAC
                                                                                                                                             TGCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAGT
                                                                                                                                                                                                                      TCAGCAGCAGAGACGAAGCCTTTCTGTAACATGCGGCCGTCCCGGCGAGAGGGGGCAGTTT
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                                                                            TTCAAGGGAGAAGGGCAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAAGCATAAGTTT
                                                                                                                    TGCTCTTTTGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAGT
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                                         TTCAAGGGAGAAGGCAAGTTTATCAAAAACATTGTTTCAGGAGAAGGGAGCATAAGTTT
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larity 99.8%;
Conservative
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/lab host="DHIOB (phage resistant)"
/clone libe"NIH MGC 46"
/clone libe"NIH MGC 46"
/clone libe"NIH MGC 46"
/clone Torgan: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
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db_xref="taxon:9606"
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Pred. No. 1.7e-247;
0; Mismatches 0;
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3401 Hillview Ave, 9
Tel: 650 354 7997
Fax: 650 354 7554
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1 (bases 1 to 729)

Scarafia,L.E., Stoufer,S.D. and Swinney,D.C.

Identification of Ring Finger proteins that interact with UbcH5a, an ubiquitin-conjugating enzyme

Unpublished (2002)
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CA916737
CA916737.1 GI:28951974
EST.
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30LSPRIM2-5A human lymphocyte Matchmaker cDNA library Homo si
cDNA clone L5 5' similar to CHFR RF; cell cycle check point,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: liliana.scarafia@roche.com
Seq_primer: matchmaker 5' AD (ctattcgatgatgaagataccccaccaaccc)
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                                                                                                                                                                                                                     CTGCAGGGCGAGAGCGTTCCTCCAGTTGTGGGTCTGGGGGGTGGTGGCATCTCCCCTAAAG
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                     AGAAGAAAATGAGAGAGGAGATGGGGACCTTGACCTGAACGGGCAGTTGTTGGTCGCACAAC
                                                                       GAAAGA
                                                                                                          GAAAGACTGCGTCCTTTTCGTCGTTGGAACCCCAGGATCAGGAGGATTTGGAGCCCGTGA
                                                                                                                                             GAAGTGGTCCCTCTGTGGCAAGTGATGAAGTCTCCAGCTTTGCCTCAGCTCTCCCAGACA
AGAAGAAAATGAGAGGAGATGGGGACCTTGACCTGAACGGGCAGTTGTTGGTCGCACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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/cell_line="EBV-transformed human peripheral blood
/cell_line="EBV-transformed human peripheral blood
/pmphocyte; B cell population; IG (+)"
/lab_host="yeast; B.coli"
/clone_lib="human lymphocyte Matchmaker cDNA library"
/clone="lib="human lymphocyte Matchmaker yeast two-hybrid sytem from Clontech; PACT has
Matchmaker yeast two-hybrid sytem from Clontech; PACT has
GAL4 AD under ADH1 promoter. This oligo-dT primed library
was screened with human UbcH5a as bait, to obtain
interacting proteins."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L5"
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Pred. No. 1.7e-244;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 690)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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601158370F1 NIH_MGC_21 Homo
                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.G.B. Consortium/LLNL at: image.llnl.gov
Plates: LLCM180 row: 1 column: 17
High quality sequence stop: 626.
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          /clone="IMAGE:3504928"
/tlssue_type="choriocarcinoma"
/tlssue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 21"
/clone_lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Site-singly cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8bb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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Query Match Best Local Similarity

18.2**%**; 99.8**%**;

Score 488; DB 2; Pred. No. 5.3e-232;

Length 690

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DEFINITION
ACCESSION
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                                                                                                                                                                                                         Transcriptome characterization elucidates signaling control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R
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17000600110226 GRN_PRENEU
CN428711 GI:47416305
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Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,
Lebkowski,J and Stanton,L.W.
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 694)
                                                                                                                                         Geron Corporation
230 Constitution Drive, Menlo
Tel: 650 473 8658
Fax: 650 473 7760
                                                                                                                                                                                               Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                              Email: rbrandenberger@geron.com
Insert Length: 694 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAACCTCGTGGAAGCATACCTCATCCAGCATCCAGACAAGAGTCGCAGTGAAGAAGAT 1215
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/tissue_type="embryonic stem cell,
mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENEU"
                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                 Location/Qualifiers
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sapiens cDNA 5', mF
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Best Local Similarity
Matches 479; Conserv
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435

420

360

375

300

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16 GGCCGCAATGTCTCTTGACAGCGGCGGCGCGCAGCCGGTTCCGGGTTCCGGCGCGGGGCCG
                                                                                                                                 TGGGGACGCTCCTGCGTCTGGGCGCGGAGGAGGCGAGCCGCACGTCCTCCTGAGGAAG
                                                                                                                                                                                                                                                         GGGATGTGAATCCCGATGGAGCGGCCCGAGGAAGGCAAGCAGTCGCCGCCGCCAGCCC
GTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGGTCAGGTGACACTGGAA
                                                                         CGGGAGTGGACCATCGGGCGGAGACGAGGTTGCGACCTTTCCCTTCCCCAGCAATAAACTG
                                                                                                                                                                        TGGGGACGGCTCCTGCGTCTGGGCGCGAGGAGGAGGGCGAAGCCGCACGTCCTCCTGAGGAAG
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                                                   Conservative
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Pred. No. 1.7e-227;
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910 b N AGENCOURT_8675647 NIH_MGC_40 Hc 5', mRNA sequence. BU148471 BU148471.1 GI:22662003 EST. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 910)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (1999) CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
CDNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LLCM2568 row: c column: 15 Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP Homo sapiens Contact: Robert Strausberg, Ph.D. Homo sapiens (human) quality sequence stop: 620. Location/Qualifiers /organism="Homo sapiens" bp Homo mRNA sapiens Consortium (LLNL) CDNA Collection (MGC) clone EST 03-SEP-2002 MAGE:6380102 ь́е

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Query Match
Best Local S
Matches 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           478;
              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                            5', mRNA sequence.
BQ887242
BQ887242.1 GI:22279256
EST.
                                                                                                                                                                                                                                                                              BQ887242 938
AGENCOURT_8670762 NIH_MGC_40
                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 938)
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cDNA Library Preparation: Rubin Laboratory
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/tissue types-carrinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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/clone_lib="MIH_MGC_40"
/note="forgan: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACAGG(s). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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Pred. No. 5.3e-227;
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REFERENCE AUTHORS TITLE

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sapiens sapiens

RESULT 21 BQ887242

DEFINITION

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SOURCE ORGANISM

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DEFINITION
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Best Local Similarity
Matches 478; Conserv
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2569 row: g column: 21
High quality sequence stop: 572.
Location/Qualifiers
BM541730.1 GI:18770627
EST.
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/clone_lib="NH10B (phage-resistant)"
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_2: EcoRI; cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:6380588"
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RESULT 23
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BX409791 Homo sapiens FETAL BRAIN Homo sapiens CSODF017YI19 5-PRIME, mRNA sequence.
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Plate: LLAM12213 row: j column: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1092)
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National Institutes of Health, Mammalian
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                                                                                                                                   TGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGACACAAGAATCCTTTG 493
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/note="Organ: uterus, vdetror: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
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|mol_type="mRNA"
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Pred. No. 1.7e-226;
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Best Local Sim
Matches 469;
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ACCESSION
VERSION
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BP 191 91006 EVRY cedex - France
EMB 191 91006 EVRY cedex - France
Int strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pcMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence belongs to sequence cluster 6792.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAF014ZC07_AF01300_2&c=6792.r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
1 (bases 1 to 909)
Li, W.B., Gruber, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX409791
BX409791.1 GI:30656946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGCAGAACATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCTCCAGCGGGAGTGTTTCTGCTGTCTGATTACAGAGTCACGGGAGACACCGTTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAATTACCTGGCAACCAGAGGTTTGACATGGAAAAAACATGTTGACCGAGAGCCTCGTGG
GGACGCAGGGTCTCCGACAGGTGCTCTGGGGGTGACTCTTCTGTGGAGCT
                                                                                       CGTGTTTTTAAAATACAGAGAGACAAGCACGTCAAGGTGTTTTCACAGCCCCCTGAGGGAAG
                                                                                                                                                                                                                          GGTTCAAAAACTAAGCATCCAGAGGCCCTGAGCAGCTTTCAGCACTGGAGGTGAAGAGAG
                                                                                                                                                                                                                                                                                                                                            GCCGCACTCAGGTGAAAGCTCACCACGCCATGAAATTCAATCATATCTGTGAACAGACAA 2071
                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGGGCCGTAACT
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                                                          CGTGTTTTTAAAATACAGAGACAAGCACGTCAAGGTGTTTTCACAGCCCCCTGAGGGAAG
                                                                                                                                                                      GGTTCAAAAACTAAGCATCCAGAGGCCCTGAGCAGCTTTCAGCACTGGAGGTGAAGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="FETAL BRAIN"
/dev stage="fetal"
/dev stage="fetal"
/clone lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDN
/note="Torgan: brain; Vector: pCMVSPORT_6; 1st strand cDN
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand CDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector. Library was not normalized."
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'db_xref="taxon:9606"
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Primates;
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; Pred. No. 1.7e-222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 909
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AUTHORS
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KEYWORDS
SOURCE
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DEFINITION
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Best Local Similarity 100.
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327 CAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCTTTACAGAC 386
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Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 824)

Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,

Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU132825
AU132825.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y., Isogai,T.)
Unpublished (2000)
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AU132825
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                                                                                                                            CATCGGGCGGAGACGATGCGACCTTTCCCTTCCCCAGCAATAAACTGGTCTCTGGAGA 266
                                                                                                                                                                           CCTGCGTCTGGGCGGAGGAGGGGGGGAGCCGCACGTCCTCCTGAGGAAGCGGGAGTGGAC
                                                                                                                                                                                                    CCTGCGTCTGGGCGGAGGAGGAGGCGAGCCGCACGTCCTGAGGAAGCGGGAGCTGGAC 206
                                                                                                                                                                                                                                                                                                                                        CTCTTGACAGCGGCGGCGCGCAGCCGGGTTCCGGGTTCCGGCGCGGGGCGGGGATGTGAAT 86
                                  CATCGGGCGGAGACGAGGTTGCGACCTTTCCTTCCCCAGCAATAAACTGGTCTCTGGAGA
                                                                                                                                                                                                                                                CCCGATGGAGCGGCCCGAGGAAGGCAAGCCGCCGCCGCCGCAGCCCTGGGGACGGCT
                                                                                                                                                                                                                                                                             CCCGATGGAGCGGCCCGAGGAAGGCAAGCAGTCGCCGCCGCCGCCGCAGCCCTGGGGACGGCT 146
                                                                                                                                                                                                                                                                                                                 CTCTTGACAGCGGCGGCGCAGCCGGTTCCGGGTTCCGGCGCGGGGGCGGGGATGTGAAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="NT2RP4"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks ratinoic acid (RA) induction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        824 bp
NT2RP4 Homo sapiens cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="NT2RP4000648"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 824
                                                                                                                                                                                                                                                                                                                                                                                    17.5%; Score 468; DB 1; Length 824; 100.0%; Pred. No. 5.3e-222; rative 0; Mismatches 0; Indels
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Db	301 CAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCTTTACAGAC 360
9	387 TGGGGATGTCATCTAGGTGTACAGGAAGAATGAACCGGGAACAACGTGGCATACCT 446
뮰	361 TGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAACCGGAACACCAACGTGGCATACCT 420
Ş	447 CTATGAATCTTTAAGTGAAAAGCAAGGCATGACACAAGAATCCTTTGA 494
Вb	421 CTATGAATCTTTAAGTGAAAAGCAAGGCATGACACAAGAATCCTTTGA 468
RESULT 25 BE257482	
LOCUS DEFINITION	BE257
ACCESSION VERSION KEYWORDS	mRNA sequence. BE257482 BE257482.1 GI:9127957 BST.
SOURCE ORGANISM	_
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	es or Healt
	Email: (20apbs remail.nih.gov Tisane Procurement: ATCC
	cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) NNA Semiencian by: Tractic Committee Tra
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov , Plate: ILCM150 row: n Column: OR
FEATURES	Ηį
source	
	/db_xref="taxon:9606" /clone="IMAGE:3352136"
	/tissue_type="retinoblastoma" /lab_host="DH10B (phage-resistant)" /cl>= lib="mur MC -te"
	/crone_rib="Nih mgc_16" /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by Oliqo-dT priming. Directionally
	<pre>cloned into BcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of in the laboratory of Gerald M. Rubin (University of</pre>
	California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
Query Matc Best Local	: -
a	06; Conservative 0; Mismatches 1; Indels 0; Gaps
Qy 1	313 TGCTGGAGCTGTCAGACGTTGACAGTGAGTCCTCAGACATTAGCCAGCC
뫄	1 recreeascrercadacerreacaereacrecercadacarradecaeccaracereere 60
200 1	1373 GCCGGCAGTGTCCTGAGTACAGAAGGCAGGCGCGGCGCAGCCTCCCCACTGCCCAGCACCCCG 1432
DЬ	61 GCCGGCAGTGTCCTGAGTACAGAAGGCAGGCGGCGCAGCCTCCCCACTGCCCAGCACCCG 120
0γ 1	.433 AGGGCGAGCAGGAGCCCCACAGGCCCTGGGGGATGCACCCTCCACGTCCGTC
DЬ	121 AGGGCGAGCCAGGAGCCCCACAGGCCCTGGGGGATGCACCCTCCACGTCCACCTGA 180

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REFERENCE
AUTHORS
TITLE
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Query Match
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BG315362
BG335362.1 GI:13141800
EST.
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                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1096)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                       quality sequence stop: 637
Location/Qualifiers
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                                                       /tissue_type="choriocarcinoma"
/lab host="DH10B (phage resistant)"
/clome lib="NIH MGC_21"
/clome lib="NIH MGC_21"
/note="Torgan: placenta; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                /mol_type="mRNA"
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                                                                                                                                                                                                                                 clone="IMAGE:4541638"
   17.0%;
99.8%;
 Score 456; DB 4;
Pred. No. 5.3e-216;
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1022 bp mRNA linear EST 20-FEB-2002
AGENCOURT_6562815 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5551112
5', mRNA sequence.
BM558904
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                              http://image.llnl.gov
Plate: LLAM12264 row: f column:
High quality sequence stop: 608.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; 1 (bases 1 to 1022)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGTCGCAGTGAAGAAGATGTGCAAAGTATGGATGCCAGGAATAAAATCACTCAAGACAT 1256
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/db_xref="taxon:9606"
/clone="IMAGE:5551112"
/tlssue_type="retinoblastoma"
                                                                                                 organism="Homo sapiens'
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                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 953)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                     5', mRNA sequence.
BQ936072
BQ936072.1 GI:22351455
Plate: LLCM2546 row: p column: High quality sequence stop: 630.
Location/Qualifiers
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                            BQ936072
AGENCOURT_8779684 NIH_MGC_18
                                                                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
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/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by
Technologies."
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Pred. No.
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5.3e-214;
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             REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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ORGANISM
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VERSION
KEYWORDS
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AGENCOURT_8853777 NIH_MGC_18
5', mRNA sequence.
BQ924736
           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
1 (Dases 1 to 938)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                            Homo sapiens (human)
                                                                                                                                                          BQ924736.1
                                                                                                                 sapiens
cgapbs-r@mail.nih.gov
```

Ьр Homo

sapiens cDNA clone

EST 20-AUG-2002 EIMAGE:6374110

Gene Collection

Euteleostomi;
; Homo.

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45 GCGCAGCCGGTTCCGGGTCGGCGCGGGGATGTGAATCCCGATGGAGCGGCCCGA
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AAAGCAAGGCATGACACAAGAATCCTTTGA
                                                           AAAGCAAGGCATGACACAAGAATCCTTTGA
                                                                                                                                                                                                        GGTGTACAGGAAGAATGAACCGGAACACAACGTGGCATACCTCTATGAATCTTTAAGTGA
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/mol type="mRNA"
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/db_xref="taxon:9606"
/clone="IMAGE:6371968"
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/tissue_type="large cell carcinoma"
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/note="Organ: lung; Vector: pOTB7; Site 1: AhoI; Site 2:
/note="Organ: lung; Vector: pO
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Pred. No. 5.3e-213;
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RESULT 30
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                       DKFZp686P03250_r1 686 (synonym: hlcc3) Homo sapiens DKFZp686P03250_5', mRNA sequence.
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BX486289.1
EST.
                                                                                                                                                                 GCAAGGCATGACACAAGAATCCTTTGA 494
                                                                                                                                                                                                                              GTACAGGAAGAATGAACCGGAACACAACGTGGCATACCTCTATGAATCTTTAAGTGAAAA 467
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/mol_type="mRNA"
/db_xref="taxon:9606"
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             GI:31949829
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Pred. No. 1.7e-211;
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JOURNAL
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Best Local Similarity
Matches 436; Conserv
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKPZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
sequencing consortium of the
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1 (bases 1 to 535)

Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
EST (Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., et al.) Unpublished (2003)

Contact: MIPS
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                                            CACAAGAATCCTTTGA
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686P03250"
/dev_stage="adult"
/lab_host="DH10B"
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/note="Vector: pTriplEx2; Site_1: SfiIA;
cDNA-collection"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
EST (Bahr,A., Lauber,J., Mewes,H.W., Weil,B., et al.)
Unpublished (2003)
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  ATGAACCGGAACACAACGTGGCATACCTCTATGAATCTTTTAAGTGAAAAGCAAGGCATGA
                                        ATGAACCGGAACACAACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGA 478
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2:
cDNA-collection"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 811)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               811 bp
AGENCOURT 13893036 NIH MGC 147 H
IMAGE:30342520 5', mRNA sequence
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                      CCCCAGCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGG
                                                                                               CGTCCTGAGGAAGCGGGAGTGGACCATCGGGCGAGACGAGGTTGCGACCTTTCCTT
                                                                                                                                                       GCCGCCGCCAGCCCTGGGGACGGCTCCTGCGTCTGGGCGCGAGGAGGAGGGCGAGCCGCA
  CCCCAGCAATAAACTGGTCTCTGGAGATCACTGTAGAATTGTAGTGGATGAAAAATCAGG
                                                                           CGTCCTCCTGAGGAAGCGGGAGTGGACCATCGGGCGGAGACGAGGTTGCGACCTTTCCTT
                                                                                                                                                                                                                                    GGTTCGGCGCGCGGGGATGTGAATCCCGATGGAGCGCCCGAGGAAGGCAAGCAGTC
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                                                                                                                                                                                                                                                                                                              16.2%; Score 435; DB 6; L
ilarity 100.0%; Pred. No. 1.7e-205;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 476.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=Torgan; placenta; Vector: pBluescriptR; Site 1: alI-XhoI; Site 2: BamH; Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                            preparation). Library constructed by M. Brownstein (NIWH/NHGRI, National Institutes of Health). Note: This is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30342520"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone lib="NIH MGC 147"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Human Placenta"
/lab_host="DH10B TonA"
                                                                                                                                                                                                                                                                                                                                                                                                              NIH_MGC library."
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268

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REFERENCE
AUTHORS
TITLE
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                                                                        Query Match
Best Local Similarity
Matches 433; Conserv
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29
                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) wit
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnll.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 806)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CB961597.1 GI:30217714
EST.
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AGENCOURT 13892092 NIH MGC 148 Homo
IMAGE:30337709 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                    TTCGGCGCGGGGGGGATGTGAATCCCGATGGAGCGGCCCGAGGAAGGCAAGCAGTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ate: NDAM363 row: d column: 06. gh quality sequence stop: 542. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAACCGGAACACAACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAGGCATGAC
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                                                                          Conservative
                                                                                                                                                                                      /clone libe WIH MGC 148"
/clone libe WIH MGC 148"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-Xho1; Site_2: BamH; Library is oligo-dT primed and
directionally Cloned using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-lenght clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pre-eclamptic
/lab_host="DH10B TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                          clone="IMAGE:30337709"
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                                                                                            Score 433;
Pred. No.
                                                                            Mismatches
                                                                                          DB 6; Lo
1.7e-204;
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sapiens cDNA clone
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                                                                                                            Length 806;
                                                                            Indels
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                                                                          Gaps
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AU154212/c
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  ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
AU154212
AU154212.1
EST.
                                                                                                                                                                                                                              1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Ozawa,M., Nishikawa,T., Nakamura,Y., Nagai,T., Sugar and Isogai,T.
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AU154212
                                                                                                                                                                                                                                                                                                                                                                                                                                            HRI human cDNA project (Ota,T., Sugiyama,T., Is Saito,K., Yamamoto,J., Ozawa,M., Nishikawa,T., Nagai,T., Sugano,S., Masuho,Y., Isogai,T.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 518)
                                                                                                                                                                                                                                                                                                                                                                Helix Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NT2RP4 Homo
                  /clone_lib="NT2RP4"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
                    cells after
                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP4000455"
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cell_line="NT2"
                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:11015733
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Primates;
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sapiens cDNA clone NT2RP4000455
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EST 05-AUG-2002

Ishii,S., Suzuki,Y.,
., Nakamura,Y., Sugano, S., Masuho, Y. Yamamoto,

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RESULT 35
AU138310
LOCUS
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AUTHORS
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JOURNAL
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Best Local Similarity
Matches 476; Conserv
                                                                           Bource
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                                                                                                                                                                                                                               COntact. Concomics Laboratory
Genomics Laboratory
Helix Research Institute
Kisarazu, Chiba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU138310
AU138310
                                                                                                   Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 687)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. an
                                                                                                                                                                                                                  1532-3 Yana, Kisarazu,
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AU138310.1
EST.
                                                                                                                                                                                                    Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                       Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                          HRI human cDNA project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLACE1
   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1008304"
                                                                                            Location/Qualifiers
                                                                           1. .687
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99.8%;
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Pred. No. 5.3e-201;
0; Mismatches 1;
                                                                                                                                                                                                                                     292-0812,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA clone PLACE1008304
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 02-AUG-2002
15', mRNA
                                                                                                                           Tokyo, and
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CN428707
LOCUS
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VERSION
KEYWORDS
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Best Local Sim
Matches 471;
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 99.8
mes 471; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 590)
Theory C. Lei S. Murage, J., Fisk, G.J.,
                                                                                                                                                                                                                Transcriptome characterization elucidates signaling networks control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
                                                                                                                                                                                                                                                                                         Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, Lebkowski, J and Stanton, L.W.
                                                                                                                           Tel: 650 473 8658
Fax: 650 473 7760
                                                                                                                                                                                 Geron Corporation
                                                                                                                                                                                                  Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CN428707.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17000600232773 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN428707
                                                                                        Imail: rbrandenberger@geron.com
Insert Length: 590 Std Error:
                                                                                                                                                               230 Constitution Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCTCAGCTCTCCCAGACAGAAAGACTGCGTCCTTTTCGTCGTTGGAACCCCAGGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAAAACCACATCCTCAACAACCTCGTGGAAGCATACCTCATCCAGCATCCA 1191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGCACGACTGCGTGAGTTTGCAGCCCTGCATGCACACGTTCTGCGCGCGGCTTGCTACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCCTCAGCTCTCCCAGACAGAAAGACTGCGTCCTTTTCGTCGTTGGAACCCCCAGGATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAAAACCACATCCTCAACAACCTCGTGGAAGCATACCTCATCCAGCATCCA
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="PL/
/note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="placenta"
/clone_lib="PLACE1"
                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:47416301
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Pred. No. 1.7e-198;
0; Mismatches 1;
                                                                                                                                                                Menlo Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PME18SFL3"
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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BQ876252
LOCUS
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ORGANISM
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AGENCOURT 8681666 NIH_MGC_43 Homo sapiens
5', mRNA sequence.
BQ876252
BQ876252.1 GI:22268258
                                                                                                                                                                                       Contact: Robert Strausberg, | Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (Dases 1 to 876)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
                                                                            CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM2559 row: o column: 18
                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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Location/Qualifiers
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/clone_lib="GRN_PREMEU"
/note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
/organism="Homo sapiens"
/mol_type="mRNA"
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Pred. No. 5.3e-198;
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KEYWORDS

FEATURES

AW957709 EST369779 AW957709

650 bp mRNA linear MAGE resequences, MAGE Homo sapiens cDNA,

mRNA sequence.

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Query Match
Best Local Similarity 99.5%;
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                                                                                      ATCCTGAAGAATTACCTGGCAACCAGAGGTTTGACATGGAAAAACATGTTGACCGAGAGC 182
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                                                                                     CN428708
17000532786421 GRN_ES Hot
CN428708
CN428708.1 GI:47416302
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 650)

Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Charles to the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: johnq@tigr.org
Plate: 110
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/clone_lib="MAGE resequences,
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100.0%; Pr.
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RESULT 40
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Best Local Similarity
Matches 414; Conserv
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                                                               17000455366473 GRN_ES
CN428710
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Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 414 Std Error:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcriptome characterization elucidates signaling control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R Regenerative Medicine
                 Homo sapiens (human)
                                                  CN428710.1
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230 Constitution Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
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/note="oligo dT primed, full-length enriched cDNA
from undifferentiated hES cell lines H1 (p32), H7
and H9 (p26) maintained in feeder-free conditions"
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/db_xref="taxon:9606"
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100.0%; Pred. No. 5.3e-195;
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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RESULT 41
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230 Constitution D
Tel: 650 473 8658
Fax: 650 473 7760
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Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R
Regenerative Medicine
                                                                  mRNA sequence. BG481936
BG481936.1 GI:13414215
EST.
                                                                                                                           BG481936
602526853F1 NIH_MGC_21 Homo
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                Homo sapiens
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Length: 614 Std Error:
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/note="oligo dT primed, full-length enriched cDNA from undifferentiated hES cell lines H1 (p32), H7 and H9 (p26) maintained in feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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E:4650348 5',
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Matches 412; Conserva
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BF109790 490 bp
7169a04.x1 Soares NSF_F8_9W_OT_I
IMAGE:3526543 3', mRNA sequence
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High quality sequence stop: 635.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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/lab host="PH10B (phage-resistant)"
/clone_lib="NIH MGC 21"
/clone_lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI; cDNA made by oligo-dr priming_
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4650348"
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Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 490)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
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Location/Qualifiers
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AATGTCACAAACTGTAGCACAAATAATATAATTTATAATTTACAAATTG 2659
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                                                                                                                                                GAAGGGAGCATAAGTTTACAGCCTACAGGACGTACACAATATCCTGCTGCTGCGGAAAACC
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/clone lib="Soares NSF F8 9W OT PA P S1"
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site=1: Not 1; Site=2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and 88 circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneIDs: Soares NDHSF pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NDZHF8-9W pool 1:
758280-760583, 772104-774407 Soares NDHPA pool 1:
758280-760583, 772104-774407 Soares NDHPA pool 1:
778270-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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90 GATGGAGCGGCCCGAGGAAGGCAAGCAGTCGCCGCCGCCGCCGCCAGCCCTGGGGACGGCTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 881)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5', mRNA sequence.
BU153737
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Plate: LLAM13464 row: a column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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AGENCOURT_7889369 NIH_MGC_67 Homo sapiens cDNA clone
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TGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGAAGCAGACATGCCCTTTACAGACTGG 389
                                                                                                                                                                                                       CGGGCGGAGACGAGGTTGCGACCTTTCCTTCCCCAGCAATAAACTGGTCTCTGGAGATCA
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                                                                                         CTGTAGAATTGTAGTGGAAAAAATCAGGTCAGGTGACACTGGAAGATACCAGCACCAG
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Location/Qualifiers
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/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life Technologies."
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/fissue_type="retinoblastoma"
/lab_host="DH10B_(phage-resistant)"
/clone_lib="NIH_MGC_67"
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/db_xref="taxon:9606"
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e IMAGE:6142354
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                                                                                                                                                                                                                                                                                               1832 CTCTCCAGCGGGAGTGTTTCTGCTGTCTGATTACAGAGTCACGGGAGACACCGTTCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
lst strand cDNA was five to NotI and cloned
into the NotI and EcoRV sites of the pcMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence belongs to sequence cluster 6792.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAF014ZC07_AF01300_1&c=6792.
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BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30656944.
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BX409790 Homo sapiens FETAL BRAIN Homo
CSDDF017YI19 5-FRIME, mRNA sequence.
BX409790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                AGAATTACCTGGCAACCAGAGGTTTGACATGGAAAAACATGTTGACCGAGAGCCTCGTGG 1831
GCCGCACTCAGGTGAAAGCTCACCACCACCACTGAAATTCAATCATATCTGTGAACAGACAA 2071
                                                                                                                 CTGCTTCCGAGTTGCCAGTGGCCGTAACATCCCGTCCTGACTGCTACTGGGGCCGTAACT
                                                                                                                                                             GTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCTGACCTATCAGTATCGGCAGAACATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-Oligo (dl) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="FETAL BRAIN"
/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0DF017YI19"
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                                                                                                                                                                                                                                                                                                                                                                                                                               386;
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1 (bases 1 to 475)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI200393 475 bp mRNA linear EST 14-Ou qf86e04.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1756926 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 474.
Location/Qualifiers
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AI200393.1 GI:3752999
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                                            TGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAGTTTTCAAGGG 2455
                                                                                                                                                                                AGAGACGAAGCCTTTCTGTAACATGCGGCCGTCCCGCCGAGAGGGGCAGTTTTGCTCTTT
                                                                                                                                                                                                                                                                                                                                GGGGGCCGCAGCCCCCCCCTGGTGAGCGCTGGGCAGGGCTCGTGGTGGCATCAGCAGC
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TGTACATTTTCCGAAACTACAGTTAAAGCAGAAGTCTGTTTTCAGGAAAAGTTTCAAGGG
                                                                                                                                        AGAGACGAAGCCTTTCTGTAACATGCGGCCGTCCCGCCGAGAGGGGGCAGTTTTGCTCTTT
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//ob_xref="taxon:9606"
//db_xref="taxon:9606"
//clone="IMAQE:1756926"
//clone="IMAQE:1756926"
//dev_stage="19 weeks"
//lab_host="PH10B (ampicillin resistant)"
//lab_host="PH
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100.0%; Pred. No. 5.3e-181;
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ORGANISM
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CN481126
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                                 Matches 436;
                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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 1806 AAACATGTTGACCGAGAGCCTCGTGGCTCTCCAGCGGGGAGTGTTTCTGCTGTCTGATTA 1865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: graeme@helix.nih.gov
Plate: 03 row: c column: 10
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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CN481126.1 GI:46562630
EST.
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hw03c10.yl Human primary human c
Homo sapiens cDNA clone hw03c10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wistow G
Section on Molecular Structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 618)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed sequence tag analysis of cultured primary human ocular
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                                 Conservative
                                                                                                         /note="Organ: Bye; Vector: pSport1; RNA was extracted from primary human pericytes in culture. A directionally cloned cDNA library in the pSPORT1 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'.pGACTAGTTCTAGATCGCAGCGCGCC(T)15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                               /clone lib="Human primary human ocular pericytes.
Unamplīfied (hw)"
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hw03c10"
                                                                                                                                                                                                                                                                                                                                             /cell_type="pericytes"
/dev_stage="Adult"
/lab_host="EMDH10B"
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                                               14.48;
                                0;
                              Score 386; DB 7;
Pred. No. 5.3e-181;
0; Mismatches 1;
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1866 CAGAGTCACGGGAGACACCGTTCTGTGTTACTGCTGTGGCCTGCGCAGCTTCCGTGAGCT 1925
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1 (bases 1 to 824)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1814 row: g column: 05 High quality sequence stop: 745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602766120F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE: 4908316
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                   /clone="IMAGE:4908316"
/tissue type="epithelioid carcinoma cell line"
/lab host="DH108 (phage-resistant)"
/clone lib="NIH_MGC_42"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT.priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5; adaptor: GGCACGAG(G). Size-selected >500
                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                         .824
average insert size 1.8kb. Library constructed by Ling
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RESULT 48
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                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Stroshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603201532F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5267575
                                                   found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM11674 row: p column: 08
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 797)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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               quality sequence stop: 793.
Location/Qualifiers
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REFERENCE
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                                                                                                                                                                                                                                                                                                            1070 bp.
AGENCOURT 6460403 NIH_MGC_88 Homo
5', mRNA sequence.
BMB0722'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                             1 (bases 1 to 1070)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
Unpublished (1999)
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                    BM802324.1
                                                                                                                                                                                                                                                                                                          BM802324
                                                                                                                                                                                                                                                 Homo sapiens (human)
cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Agencourt Bioscience Corporation
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/clone lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified /note="Organ: testis; Vector: pBluescriptR (z SalI-XhoI pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (qtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 1.7e-178;
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                                                                                                                                   Gene Collection (MGC)
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MAGE:5559833
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REFERENCE
AUTHORS
TITLE
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KEYWORDS
SOURCE
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BE407797
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                                       COMMENT
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Best Local Simi
Matches 364;
                                                                                                                                                                 ORGANISM
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                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Butheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 636)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                   mRNA sequence. — — BE407797 BE407797.1 GI:9344247 EST.
                                                                                                                                                                                                                                                             BE407797
601299183F1 NIH_MGC_21 Homo
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Plate: LLAM12285 row: a column: 18
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/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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/clone_lib="NHH_MGC_88"
/clone_unidirectionally;
Site_1: NotI; Site_2: Sali; Cloned unidirectionally;
Oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC_Library."
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/db_xref="taxon:9606"
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Location/Qualifiers
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                         ACGGCGTGCTGAACAACAACAGCTACGAGTCAGACAT 1766
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/mol type="mRNA"
/mol type="mRNA"
/db Xxef="taxon:9606"
/db Xxef="taxon:9606"
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/clone lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Site_inally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/cgm2_6/ptodata/1/ina/5B_COMB.seq:*
/cgm2_6/ptodata/1/ina/6B_COMB.seq:*
/cgm2_6/ptodata/1/ina/6B_COMB.seq:*
/cgm2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgm2_6/ptodata/1/ina/backfiles1.seq:*
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5198347-3
US-09-614-912-161
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US-09-412-102-1
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US-08-714-524D-35
US-09-270-767-231495
US-09-270-767-2319
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Sequence 18, Application US/07847010 Patent No. 5693495
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compartible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/847,010

FILING DATE: 01-JUN-1992

CLASSIFICATION: 435
     TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                              ATTORNEY/AGENT INFORMATION:
NAME: JORGE III, HARTY C
REGISTRATION UNMERR: 20,280
REFERENCE/DOCKET NUMBER: 6530-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEPAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ferreira, Fatima
TITLE OF INVENTION: Allergens of Alder Pollen and
TITLE OF INVENTION: Applications Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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US-09-482-273-73

US-09-49-847-14

US-09-270-767-9995

US-09-149-476-127

US-08-820-170A-12

US-09-055-699-12

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US-09-273-565-12

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US-09-661-468-12

US-09-976-165-12
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US-09-178-115-90

US-09-177-776-90

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US-09-248-796A-11988
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT FILING NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 11988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Yalpani, Nasser
TITLE OF INVENTION: Maize Chitinases and Their Use in
TITLE OF INVENTION: Maize Chitinases and Their Use in
TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
FILE REFERENCE: 1100
CURRENT APPLICATION NUMBER: US/09/522,714
CURRENT FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/125,915
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                     Sequence 11988, Application US/09248796A Patent No. 6747137
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LOCATION: (46)...(966)
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ORGANISM: Zea mays
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LIBRARY: POLLEN FROM ALLERGON AB,
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ORGANISM: hazel (Corylus sp.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity es 26; Conserv
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llarity 100.0%;
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100.0%; Pred. No. 0.57;
7ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1085;
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RESULT 1 US-07-847-010-18/c

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

STREET:

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ADDRESSEE:

COUNTRY: U.S.A.

New York

APPLICANT:

INFORMATION:

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; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-11988
US-09-614-912-161
Sequence 161, Application US/09614912
Patent NO. 6677502
GENERAL INFORMATION:
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                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17572
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5198347-3
;Patent No. 5198347
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                                                            RESULT 6
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , APPLICANT: Miller, LO, DAVIC C., FANG, XIANGDOUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:3:
                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 17572
LENGTH: 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17572, Ap
Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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                                                                                                                                                                   23;
                                                                                                         TTGACAMAAAAAAAAAAAAAAAA 442
                                                                                                                                                                  0.9%; Score 23; ilarity 100.0%; Pred. No. Conservative 0; Mismatci
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Pred. No. 1.6;
0; Mismatches
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RESULT 7
US-09-412-102-1
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PATENT NO. 62227
PATENT NO. 62227
PATENT NO. 62227
PAPPLICANT: JESSEN, HOLLY J
APPLICANT: MEYER, TERRY E

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LENGTH: 1185
TYPE: DNA
ORGANISM: Glycine max
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Best Local
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-12-21
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SOFTWARE: Microsoft
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                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/412,102
ATTORNEY/AGENT INFORMATION: NAME: Spruill, W. Murray
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Local 5.
23;
                                                                                                                                                                                                                              FILING DATE:
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ZIP: 27622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Raliegh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP) STREET: 3605 Glenwood Ave. Suite 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1163 TTGACAAAAAAAAAAAAAAA 1185
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INVENTION: Plant Metabolism Genes
ERENCE: BB1378 US NA
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Weng, Zude
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Orozco, Buddy
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100.0%; Pred. No. 3.
ive 0; Mismatches
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REGISTRATION NUMBER:

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Best Local Similarity
Matches 23; Conserv
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APPLICANT: JESSEN
APPLICANT: MEYER,
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/
FILING DATE:
FILI
                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEPAX: 919 881 3175
TELEPAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 1:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1347 base pair
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ORIGINAL SOURCE:
ORGANISM: Zea m
IMMEDIATE SOURCE:
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1347 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                          MOLECULE TYPE: O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: JESSEN, HOLLY J
APPLICANT: MEYER, TERRY E
TITLE OF INVENTION: GENES AND METHODS FOR CONTROL OF
TITLE OF INVENTION: NEMATODES IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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ORGANISM: Zea mays
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                                                                                                                                                          STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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                                                               Best Local Similarity Matches 23; Conserv
                                                                                               Query Match
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Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/
FILING DATE: 01-JUL-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,101B
FILING DATE: 07-UN-1995
CLASSIFICATION: 800
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 01-JUL-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
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LOCATION:
                                                                                                                                                                                                                                                                                                                                           NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801 REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                 TYPE:
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                                                                                                                                                                                                                                               LENGTH: 2405 base pairs
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                                                                Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                               288..2196
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                                                                                                                                                                                                                  double
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100.0%; Pred. No. 3.9;
ative 0; Mismatches
                                                                                0.9%; Score 23;
100.0%; Pred. No.
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                                                                Mismatches
                                                                                  DB 1;
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RESULT 11
US-08-714-524D-35
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; LOCATION:
US-08-484-101B-49
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US-08-484-101B-49
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Best Local Similarity
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                                                                                                                GENERAL INFORMATION:
                                                                                                                                Sequence 35, Application US/08714524D Patent No. 6294716
                                                                                                                                                                                                                                                                                                                            Matches
              APPLICANT: Meyerowitz, Elliott M
APPLICANT: Chang, Caren
APPLICANT: Bleecker, Anthony B
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
FILE REFERENCE: a-57515-4
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CURRENT APPLICATION NUMBER: US/08/714,524D
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TELEPAX: (415) 398-3249
NFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57515-2/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F
REGISTRATION NUMBER: 31,80
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APPLICATION NUMBER: 1
FILING DATE: 01-JUL-
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TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
TITLE OF INVENTION: ETHYLENE
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FILING DATE: 07-JUN-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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FILING DATE: 01-JUL-1994
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3400 Embarcadero Center, Suite 3400
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100.0%; Pred. No. 3.7;
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US-09-270-767-8213
; Sequence 8213, Application US/09270767
; Patent No. 6703491
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                                                    ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8213
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US-08-714-524D-49
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                                                                                                                GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: HOmburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF ERQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8213
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SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 35. 1
LENGTH: 2405
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LENGTH: 2405
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Query Match
Best Local Similarity
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APPLICANT: Bleecker, Anthony B
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
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NAME/KEY: CDS
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NAME/KEY: CDS
LOCATION: (288)..(2195)
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100.0%; Pred. No.
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RESULT 14
US-09-270-767-23495
; Sequence 23495, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23495:
LENGTH: 121
                                                                              CLASSIFICATION: 530
CLASSIFICATION: CO7K 7
CLASSIFICATION: A61K 37
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT
FILING DATE: 19-NOV-199
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18,
Patent No. 5
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                        SOFTWARE: WordPerfect version 5.1 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.0
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TITLE OF INVENTION: leeches.
NUMBER OF SEQUENCES: 23
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                                                                SEQUENCE CHARACTERISTICS:
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            LENGTH: 277 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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1101 Connecticut Avenue
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                                                                                                                                                                                                                                                                                                                                                              USA
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Kroeger, Burkhard
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C07K 73/10
A61K 37/64
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RESULT 18
US-09-205-258-172
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US-09-311-021-161
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TITLE OF INVENTION: Nucleic Acid Molecules Encoding
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 159
LENGTH: 424
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SEQ ID NO 161
LENGTH: 622
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APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Agostino, Michael J.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6300-11A
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/311,021
CURRENT FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 268
                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 172, Application US/09205258
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ITLE OF INVENTION: 207 Human Secreted Proteins
                                    APPLICATION NUMBER: 60/048,949
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,974
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,883
                                                                                                                                                                                                     RILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
RILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,875
RILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,964
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APPLICATION NUMBER: 60/048,876
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,897
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APPLICATION NUMBER: 60/048,916
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; SOPTWARE: PatentIn Ver. 2
; SEQ ID NO 172
; LENGTH: 786
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-205-258-172
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; ORGANISM: Drosophila melanogaster
US-09-270-767-5937
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US-09-270-767-21219
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21219
LENGTH: 809
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Patent No. 6703491
GENERRAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
                                                                                                                                                                           Sequence 21219, Appl Patent No. 6703491 GENERAL INFORMATION:
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SEQ ID NO 5937
LENGTH: 809
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 62517
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EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
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FILING DATE: 1997-06-06
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100.0%; Pred. No.
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tive 0; Mismatc
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; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-21219
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Best Local
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APPLICATION NUMBER: 60/048,882
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
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APPLICATION NUMBER: 60/048,892
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FILING DATE: 1997-06-06
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FILING DATE: 1998-06-04
                                                                              FILING DATE: 1997-06-06
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RESULT 22 US-09-475-316A-24

Sequence

Sequence 24, Application US/09475316A Patent No. 6210942

APPLICANT: APPLICANT:

Lewis, No. 6210942man G. Davin, Laurence B.

Albena T

APPLICANT: APPLICANT:

Gang, David R. Sarkanen, Simo Ford, Joshua D

Fujita, Masayuki Dinkova-Kostova,

APPLICANT: Sarkanen, Simo
APPLICANT: Ford, Joshua D
TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICIRESINOL REDUCTASES,
TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE
FILE REFERENCE: WSUR-1-13793

CURRENT APPLICATION NUMBER: US/09/475,316A CURRENT FILING DATE: 1999-12-30

PRIOR APPLICATION NUMBER:

GENERAL INFORMATION:

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                                                                                                                                 ; OTHER INFORMATION: US-09-205-258-190
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. SEQ ID NO 190
                                                                Matches
                                                                                            Query Match
                                                                                                                                                               FEATURE:
NAME/KEY: SITE
LOCATION: (145)
                                                                                                                                                                                                                              FEATURE:
NAME/KEY: SITE
LOCATION: (144)
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1227
                                                                                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1998-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
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EARLIER
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EARLIER APPLICATION NUMBER: 60/070,923
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                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                 OTHER INFORMATION:
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                                                                              Local
                   2657 TTGACAAAAAAAAAAAAAAAAAA 2678
843 TTGACAAAAAAAAAAAAAAAAAAA 822
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APPLICATION NUMBER: 60/048,883
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                                                              l Similarity
22; Conserv
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                                                             0.8%; Score 22; llarity 100.0%; Pred. No. Conservative 0; Mismatc
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PRIOR FILING DATE:

1999-05-07

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RESULT 23
US-09-704-640-24
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Best Local Similarity
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 09/475,316
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 09/307,653
PRIOR FILING DATE: 1999-05-07
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NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/704,640
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                                                                                                                                                                         TYPE: DNA
ORGANISM: Thuja plicata
                                                                                                                            NAME/KEY: CDS
LOCATION: (94)..(669)
                                                                                                                                                            FEATURE:
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LOCATION: (94)..(669)
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ORGANISM: Thuja plicata
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                        2657 ТТСАСААААААААААААААА 2678
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6635459
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Sarkanen, Simo
Ford, Joshua D
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Fujita, Masayuki
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                                                       Conservative
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100.0%; Pred. No.
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                                                        Mismatches
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US-09-183-861-19
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Best Local :
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                                                                                              Patent No. 6375955
GENERAL INFORMATION:
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                                                                                                                               Sequence 19, Application US/09022765
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                                                               APPLICANT: Reed, Steven G. APPLICANT: Campos-Neto, An
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
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LENGTH: 1019 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                             Local
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LOCATION:
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                                                                                                                                                                                                                                                                                                Similarity
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Skeiky, Yasir A.W.
               Dillon, Davin C.
Skeiky, Yasir A.W.
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                                                Webb, John R
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71..523
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LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
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100.0%; Pred. No.
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NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

STREET:

6300 Columbia Center, 701 Fifth Avenue

SEED and BERRY LLP

ADDRESSEE:

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; FEATURE:
; NAME/KEY:
; LOCATION:
US-09-022-765-19
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US-09-551-974A-19
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                                                                          US-09-551-974A-19
                                                                                                                       CURRENT APPLICATION NUMBER: US/09/551,974A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-198
CLASSIFICATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Appl Patent No. 650043
Query Match 0.8
Best Local Similarity 100.
Matches 22; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                  APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 base pairs
                                                                                       TYPE: DNA
ORGANISM: Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: ORIGINAL SOURCE: ORGANISM: Lei
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Campos-Neto, Antonio
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   Gaps
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US-09-639-206A-19
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US-09-565-501A-19
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                                                                                                                      US-09-639-206A-19
                                           Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/639,206A
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
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SEQ ID NO 19
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/565,501A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                       APPLICANT: PROBST, PECET TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS FILE REFERENCE: 210121.420C7
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, A
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                                                                                                                                  LENGTH: 1019
TYPE: DNA
ORGANISM: Leishmania major
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2658 TGACAAAAAAAAAAAAAAAA 2679
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Skeiky, Yasir A.W.
Bhatia, Ajay
Coler, Rhea
Coter Probst
Peter Probst
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                                                  0.8%; Score 22; DB llarity 100.0%; Pred. No. 10 Conservative 0; Mismatches
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                                                                   DB 4;
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US-09-874-923-19
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APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Probst, Peter
APPLICANT: Brannon, Mark
APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEIS!
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEIS!
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 1019
TYPE: DNA
ORGANISM: Leishmania major
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Best Local (
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                                                                                                                                                                                 ZIP: 98104-7092
COMPUTER: FLORDY disk
COMPUTER: FLORDY DISK
COMPUTER: SYSTEM: PC-DOS/MS-DOS
ODERATING SYSTEM: Release #1.0, V6
CURRENT APPLICATION DATA:
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APPLICANT: Corixa
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CURRENT FILING DATE: 2001-06-04
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APPLICANT: Campos-Neto, Antonio
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TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
                                                   TELECOMMUNICATION INFORMATION:
                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                  TELEPHONE:
                                                                   NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                    APPLICATION NUMBER: US/08/798,841 FILING DATE: 12-FEB-1997 CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
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Skeiky, Yasir A.W.
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                      (206)
     206) 682-6031
SEQ ID NO: :
                                    (206)
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                                    622-4900
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Pred. No. 10;
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Patent No. 6300096
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Glameno, Ruth B.
APPLICANT: Glameno, Ruth B.
APPLICANT: Tartaglia, Louis A.
ITILE OF INVENTION: FAITY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-21p3MA
CURRENT APPLICATION NUMBER: US/09/232,197A
CURRENT FILING DATE: 1999-01-14
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US-09-232-197-50
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US-09-232-200-50
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Best Local 9
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SEQ ID NO 50
LENGTH: 1173
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Sequence 50, App-
Sequence 50, App-
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CURRENT APPLICATION NUMBER: US/09/232,200A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
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TITLE OF INVENTION: FATTY ACID TRANSPORT PROTBINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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les 22; Conserv
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71..523
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100.0%; Pred. No.
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100.0%; Pred. No.
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                                                                                                                                                                                                                                     RESULT 34
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                GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Codish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-21p3MD
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SEQ ID NO 50
LENGTH: 1173
                                                                                                                                                                        Sequence 50, Application US/09232195A Patent No. 6657049
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SEQ ID NO 50
LENGTH: 1173
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Best Local Similarity
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER FPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER ALLING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: WHI97-21p3MC
CURRENT APPLICATION NUMBER: US/09/232,201A
CURRENT FILING DATE: 1999-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: US/09/232,195A
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100.0%; Pred. No.
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.00.0%; Pred. No.
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RESULT 35
US-09-064-411A-35
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SEQ ID NO 50
LENGTH: 1173
                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,411A
FILING DATE: 22-ARR-1998
CLASSIFICATION BOD
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,827
FILING DATE: 05-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BOTUCKI, Andrea T.
REGISTRATION NUMBER: 33651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, Application US/09064411A Patent No. 6331664
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Best Local Similarity 100.0%; P
Matches 22; Conservative 0;
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EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/03,491
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Skokut, Tom
APPLICANT: Young, Scott
APPLICANT: Folkerts, Otto
APPLICANT: Armstrong, Katherine
APPLICANT: Cowen, Neil M.
TITLE OF INVENTION: Mucleotide Sec
TITLE OF INVENTION: Thioesterase a
TITLE OF INVENTION: Their Use In Thumber of Sequences: 49
                                                                                               TELEFAX: 317-337-4847
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                            REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dow AgroSciences Patent Department STREET: 9330 Zionsville Road CITY: Indianapolis
                     TOPOLOGY:
                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                              LENGTH:
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                                                    nucleic acid
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                                                                              1287 base pairs
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                                    single
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Thioesterase and Palmitoyl-ACP Thioesterase Genes and
Their Use In The Regulation of Fatty Acid Content of Oil
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LOCATION: 58...510
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SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-08-979-608A-10
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Best Local S
                                Query Match
Best Local Similarity
Matches 22; Conserv
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GENERAL INFORMATION:
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NAME/KEY:
LOCATION:
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APPLICATION NUMBER: US/08/979,608A

FILING DATE: 26-NG. 6355451-1997

PRIOR APPLICATION DATA:

APPLICATION UNMBER: US 60/048,547

FILING DATE: 03-JUN-1997

APPLICATION NUMBER: US 60/031,930

PILING DATE: 27-NOV-1996
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Fish & Richardson P.C.
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2657 TTGACAAAAAAAAAAAAAA 2678
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22; Conservative (
                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                              NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
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                                                                                                                                                                                       TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                        LENGTH: 1404 base pairs
                                                                                                                                                                                                                                                                                          TELEFAX: 617/542-8906
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140..1135
                                   Conservative
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38..1135
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                                                0.8%; Score 22; DB 3;
100.0%; Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robert S.
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                                   Mismatches
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                                                                 Length 1404;
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RESULT 38
US-09-616-289-10
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                                                                                        GENERAL INFORMATION:
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Best Local Similarity
Matches 22; Conserv
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Patent No. 6605588
GENERAL INFORMATION:
                                                                                                   Sequence 10, Appli
Patent No. 6632923
                                                      APPLICANT: Lees, Ann M. APPLICANT: Lees, Rober
                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Coding Sequence
LOCATION: 58...510
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                    1383 TTGACAAAAAAAAAAAAAAAA 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USES TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lees, Ann M.
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ADDRESSEE: Fish & Richardson P.C.
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I: Lees, Robert S.
I: Law, Simon W.
I: Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
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                                                                                                                    Application US/09616289
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                                                                                                                                                                                                                                                                               0.8%; Score 22;
100.0%; Pred. No.
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10;
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RESULT 40
US-09-268-140-11
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CURRENT APPLICATION NUMBER: US/09/616,289

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR PILING DATE: 2000-03-02

PRIOR PPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR PPLICATION NUMBER: US 60/031,930

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR PILING DATE: 1996-11-27

PRIOR PILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

NUMBER OF SEQ ID NOS: 53
            GENERAL INFORMATION:
APPLICANT: Gemmill, Robert M.
APPLICANT: Drabkin, Harry A.
APPLICANT: Drabkin, Harry A.
TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Applica
Patent No. 6576814
GENERAL INFORMATION:
                                                                                                                    Sequence 11, Application US/09268140 Patent No. 6268176
                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 22; Conserv
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Matches 22; Conserv
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SEQ ID NO 10
LENGTH: 1404
                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Briggs, Steven
TITLE OF INVENTION: An anipulation of Mlo Genes to
TITLE OF INVENTION: An Plants
FILE REFERENCE: 5718-42035718/158714
CURRENT APPLICATION NUMBER: US/09/347,650
CURRENT FILLING DATE: 1999-07-06
CURRENT FILLING DATE: 1999-07-06
MUMBER OF SEQ ID NOS: 20
CURRENT APPLICATION NUMBER: US/09/268,140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: Mlo9
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
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                                                                                                                                                                                                                                                                   2658 TGACAAAAAAAAAAAAAAAAAA 2679
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                                                                                                                                                                                                                                         TGACAAAAAAAAAAAAAAAA 1552
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                                                                                                                                                                                                                                                                                                                                       100.0%;
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                              0.8%;
                                                                                                                                                                                                                                                                                                                                            Score 22;
; Pred. No.
                                                                                                                                                                                                                                                                                                                       0; Mismatches
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2658 TGACAAAAAAAAAAAAAAAAA 2679

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; TYPE: DNA; Homo sapiens US-09-268-140-11
                                                                         ; ANTI-SENSE:
US-07-867-106-5
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                                                                                                                                                                    TELEFAX: 215-200 - S:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
FRIGHT: 2422 base pairs
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SEQ ID NO 11
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
PILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.8%; Score 22; Best Local Similarity 100.0%; Pred. No. Matches 22; Conservative 0; Mismatc
   Matches
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GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/077,723
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                           NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE
TBLECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Improved Plasmid Vectors for Cellular TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith
                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                    TOPOLOGY:
                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEB: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
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0.8%; Score 22;
larity 100.0%; Pred. No.
Conservative 0; Mismatc
                                                                                                                                  circular
                                                                                                              DNA (genomic)
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   Mismatches
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                                     DB 1;
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                                   Length 2422;
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   Indels
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2295 TGACAAAAAAAAAAAAAAAA 2274

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US-09-604-605-1
; Sequence 1, Application US/09604605
; Patent No. 6421613
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                                                         RESULT 44
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                                                                                                                                                                                                                                                                     , NAME/KEY: repeat_unit
; LOCATION: (165)...(176)
US-09-268-140-7
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; LOCATION: (238)..(2232)
US-09-268-140-1
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Best Local Similarity 100.0%; P
Matches 22; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09268140
Patent No. 6268176
GENERAL INFORMATION:
APPLICANT: Genmill, Robert M.
APPLICANT: Drabkin, Harry A.
TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED FILE REFERENCE: 93445-00004
                                                                                                                                                                                           Matches
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Gemmill, Robert M.
APPLICANT: Drabkin, Harry A.
APPLICANT: Drabkin, Harry A.
TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED FILE REFERENCE: 93445-00004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09268140 Patent No. 6268176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/268,140
CURRENT FILING DATE: 2000-03-12
PRIOR APPLICATION NUMBER: US 60/077,723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/268,140
CURRENT FILING DATE: 2000-03-12
PRIOR APPLICATION NUMBER: US 60/077,723
PRIOR FILING DATE: 1998-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2517
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                                                                                                                                                     2658 TGACAAAAAAAAAAAAAAAA 2679
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                                                                                                                 TGACAAAAAAAAAAAAAAA 2516
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1998-03-12
                                                                                                                                                                                                         0.8%; Score 22; DB 3;
100.0%; Pred. No. 9.7;
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100.0%; Pred. No. 9.7;
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                                                                                                                                                                                           Mismatches
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; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (110)...(2269)
US-09-604-605-1
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US-08-160-861-1
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US-08-160-861-1
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SEQ ID NO 1
LENGTH: 2533
                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/160,861
FILING DATE: 02-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
DECLOPPORTON. NUMBER: 36217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5529295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity 100.0%;
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                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/604,605
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/143,222
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ramgopal Nadimpalli
APPLICANT: Carl R. Simmons
TITLE OF INVENTION: Maize Prol:
FILE REFERENCE: 1138
                                                                                                                                                                                                                    REGISTRATION NUMBER: 36217
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
                                                      FEATURE:
                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                        LENGTH: 2608 base partyPE: nucleic acid STRANDEDNESS: both TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C. 20005
                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: STERNE, KESSLER, GOLDSTEIN & FOX
1100 NEW YORK AVE NW SUITE 600
                                                                                                                                            2608 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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100.0%; Pred. No.
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Query Match

0.8%;

Score 22;

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Length 2608;

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RESULT 47
US-07-867-106-4/c
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US-10-140-002-345
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Best Local Similarity
Matches 22; Conserv
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 345
LENGTH: 2933
TYPE: DNA
                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/07867106
Patent No. 5389526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                         APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                       COUNTRY: USA
ZIP: 19103
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5. 6725730
                                                                                                          Philadelphia
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Filvaroff,Ellen
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100.0%; Pred. No.
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RESULT 48
US-07-867-106-2
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Best Local Similarity
Matches 22; Conserv
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GENERAL INFORMATION:
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                                                                            APPLICATION NUMBER: US/07/867,106
FILING DATE: 19320625
PRIOR APPLICATION DATA: APPLICATION DATA: AU DJ 7187
APPLICATION NUMBER: AU DJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
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SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
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NAME: Feeney, Joanne Longo REGISTRATION NUMBER: 35,134 REFERENCE/DOCKET NUMBER: RITELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Improved Plasmid Vectors for Cellular TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium NUMBER OF SEQUENCES: 19
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APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith
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One Liberty Place 46th Floor
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                                           RICE-0002
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APPLICALL...

PILING DATE: 02-NOV-1>0.

ATTORNEY/AGENT INFORMATION:

NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134

REFERENCE/DOCKET NUMBER: RICE-0002

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
FELEPAX: 215-568-3100
FILEPAX: 215-568-3100
FILE
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Best Local Similarity
Matches 22; Conserv
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APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
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LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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CURRENT APPLICATION DATA:
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                                                                                             MOLECULE TYPE:
ANTI-SENSE: NO
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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CITY: Philadelphia
STATE: PA
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
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One Liberty Place 46th Floor
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2378..5038
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US-08-836-022A-10
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APPLICANT: Trustee,
APPLICANT: Wilson,
APPLICANT: Fisher,
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                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/836,022A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/331,381
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVFN.008P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                              TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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TITLE OF INVENTION: Improved Adenovirus Virus and
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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STATE: Pennsylvania
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; SEQ ID NO 1 ; LENGTH: 1995 ; LENGTH: 1995 ; TYPE: DNA ; ORGANISM: HOMO SAPIENS US-09-780-525-1 Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1995; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1995; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1995; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1995; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1995; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	P-70668-C1 ON NUMBER: US/09/780, TE: 2001-02-09 NUMBER: 09/456,876 :: 1999-12-08 NOS: 2 for Windows Version	Patent No. US20020004223A1 GENERAL INFORMATION: APPLICANT: Bin-Bing Zhou APPLICANT: Yuan Zhu APPLICANT: Priya Chaturvedi APPLICANT: Mark R. Hurle APPLICANT: Miaotong Li TITLE OF INVENTION: FLARI, A NEW RING FINGER PROTEIN	RESULT 1 US-09-780-525-1 . Semience 1. Application US/09780525	ALIGNMENTS ALIGNMENTS	22 0.8 2074 18 US-10-425-115-120235 Sequence 22 0.8 2104 18 US-10-739-930-845 Sequence 22 0.8 2173 18 US-10-723-860-1885 Sequence 22 0.8 2187 9 US-09-984-245-93 Sequence	c 992 22 0.8 2000 11 US-09-938-842A-4010 Sequence 4010, Ap 993 22 0.8 2000 11 US-09-938-842A-4017 Sequence 4017, Ap 994 22 0.8 2000 11 US-09-938-842A-4773 Sequence 4773, Ap 995 22 0.8 2000 11 US-09-938-842A-5013 Sequence 5013, Ap	22 0.8 2000 9 US-09-938-842A-4017 Sequence 22 0.8 2000 9 US-09-938-842A-4773 Sequence 22 0.8 2000 9 US-09-938-842A-5013 Sequence 22 0.8 2000 11 US-09-938-842A-3674 Sequence	22 0.8 1986 18 US-10-425-115-174166 Sequence 22 0.8 1987 16 US-10-264-237-115 Sequence 22 0.8 2000 9 US-09-938-842A-3674 Sequence 22 0.8 2000 9 US-09-938-842A-4010 Sequence	22 0.8 1946 10 US-09-822-846-263 Sequence 22 0.8 1964 14 US-10-223-076-14 Sequence 22 0.8 1979 18 US-10-723-860-6704 Sequence 22 0.8 1982 18 US-10-739-930-1030 Sequence	22 0.8 1768 10 US-09-997-003-20 Sequence 22 0.8 1795 18 US-10-425-115-127167 Sequence 22 0.8 1803 18 US-10-723-860-5943 Sequence 22 0.8 1824 18 US-10-425-115-46816 Sequence	22 0.8 1665 18 US-10-425-115-32818 Sequence 22 0.8 1676 18 US-10-425-115-35855 Sequence 22 0.8 1752 18 US-10-425-115-91391 Sequence 22 0.8 1757 18 US-10-425-115-125815 Sequence	22 0.8 1641 14 US-10-372-876-108 Sequence 22 0.8 1641 15 US-10-372-876-108 Sequence 22 0.8 1641 15 US-10-372-876-108 Sequence 22 0.8 1650 17 US-10-767-701-14815 Sequence	964 22 0.8 1574 17 US-10-437-963-64454 Sequence 965 22 0.8 1597 16 US-10-416-330-5 Sequence 966 22 0.8 1597 16 US-10-287-971-99 Sequence 967 22 0.8 1506 16 US-10-287-371-664 Sequence 967 22 0.8 1606 16 US-10-264-237-664	22 0.8 1486 13 US-10-010-050A-1 Sequence 22 0.8 1489 18 US-10-739-930-2786 Sequence
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RESULT 2
US-10-108-260A-2073
| Sequence 2073, Application US/10108260A
| Publication No. US20040005560A1
| GENERAL INFORMATION:
| APPLICANT: HELIX RESEARCH INSTITUTE
| TITLE OF INVENTION: No. US20040005560A1e1 full length
| FILE REFERENCE: H1-A0106
| CURRENT APPLICATION UNWBER: US/10/108,260A
| CURRENT FILING DATE: 2002-03-27
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99.9%;
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RESULT 3
US-09-764-864-22
IS-09-764-864-22
; Sequence 22, Application US:
; Patent No. US20020132753A1
; GENERAL INFORMATION:
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; OTHER INFORMATION: n equals a,t,g, or US-09-764-864-22
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
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Best Local Similarity
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
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ORGANISM: Homo sapiens
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                                                                       CAGACAAGAGTCGCAGTGAAGAAGATGTGCAAAGTATGGATGCCAGGAATAAAATCACTC
                                                                                                                         AGCGGATCTGTAAAAACCACATCCTCAACAACCTCGTGGAAGCATACCTCATCCAGCATC 1189
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Pred. No.
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APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITIE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: UP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 160
LENGTH: 2186
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US-10-094-749-160
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APPLICANT: ISOGAI, I
APPLICANT: SUGIYAM
APPLICANT: OTSUKI,
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Best Local Similarity
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMBCHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
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YAMAMOTO, JUN-ICHI
ISONO, YUUKO
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o. US20030219741A1
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nilarity 99.7%;
Conservative
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Pred. No. 2.7e-310;
0; Mismatches 1;
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WS-09-764-864-483

(US-09-764-864-483)

(Sequence 483, Application US/09764864)

(Patent No. US20020132753A1)

(GENERAL INFORMATION:

(APPLICANT: Rosen et al.

(TITLE OF INVENTION: Nucleic Acids, Proteins, and FILE REFERENCE: PTZ23

(CURRENT APPLICATION NUMBER: US/09/764,864)

(CURRENT FILING DATE: 2001-01-17
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SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 483
LENGTH: 693
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
            NAME/KEY: SITE
LOCATION: (11)
OTHER INFORMATION: n eo
NAME/KEY: SITE
LOCATION: (13)
OTHER INFORMATION: n eo
NAME/KEY: SITE
LOCATION: (623)
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                                    APPLICANT: Rosen et al.
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, an
FILE REFERENCE: PT223
CURRENT APPLICATION UMMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM o
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 322
LENGTH: 357
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
NAME/KEY: SITE
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US-09-764-864-322
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US-09-764-864-483
                                                                                                                                                                                                                                                 Sequence 322, Application US/09764864 Patent No. US20020132753A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 455; Conserv
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OTHER INFORMATION:
NAME/KEY: SITE
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OTHER INFORMATION:
NAME/KEY: SITE
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NAME/KEY: SITE
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OTHER INFORMATION: n
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LOCATION: (640)
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100.0%; Pred. No. 6.6e-220;
tive 0; Mismatches 0;
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US-09-764-864-322
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US-09-764-864-323
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Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 238; Conserv
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SEQ ID NO 323
LENGTH: 354
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Best Local !
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: SITE
LOCATION: (313)
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NAME/KEY: SITE
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CGGAACACAACGTGGCATACCTCTATGAATCTTTAAGTGAAAAGCAAAGGCATGACACA 482
                                                                      AGCAGACATGCCCTTTACAGACTGGGGATGTCATCTACTTGGTGTACAGGAAGAATGAAC 424
                                                                                                            TGACACTGGAAGATACCAGCACCAGTGGAACAGTGATTAACAAGCTGAAGGTTGTTAAGA
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100.0%; Pred. No.
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Pred. No. 1.9e-124;
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RESULT 9
US-09-918-995-13662
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US-09-764-864-742
                                                                                                                                                 FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 13662
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13662, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 742
LENGTH: 354
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                       APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
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LOCATION: (289)
OTHER INFORMATION: I
NAME/KEY: SITE
LOCATION: (313)
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
NAME/KEY: misc_feature
LOCATION: (1)...(449)
OTHER INFORMATION: n =
                                                                   TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2180

TENGTH: 476
                                                                                                                                                                                              RESULT 11
US-09-908-975-6220
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US-09-918-995-2180
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Sequence 6220, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Publication No. US20030073623A1
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Best Local Similarity
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NAME/KEY: misc_feature
LOCATION: (1)...(476)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.0%; tes 77; Conservative 0
                                                                                                                                                                                                                                                                                                                    2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2625 TAGCACAAATAATATATATATATTTACAAATTGAC 2661
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100.0%; Pr/
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 5.6e-2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                        TRANSCRIPTS
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                        AND
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                        SPLICE
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CURRENT APPLICATION NUMBER: US/09/908,975;
CURRENT FILING DATE: 2001-07-20;
PRIOR APPLICATION NUMBER: US 60/287,724;
PRIOR ETILING DATE: 2001-05-02;
PRIOR APPLICATION NUMBER: US 60/221,607;
PRIOR FILING DATE: 2000-07-28;
NUMBER OF SEQ ID NOS: 32337;
SOPTWARE: Patentin version 3.0;
SEQ ID NO 6220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication M. GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

FIITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FITTLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

FILE REFERENCE: 38-21(53222)B

FURRENT APPLICATION NUMBER: US/10/425,115
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                                                                                                                                                                                                                                                                                                                         RESULT 13
US-10-719-993-23863/c
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                                                    Sequence 23863, Application US/10719993

Publication No. US20040265849A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALCHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001496

FULL REFERENCE: CL001496

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT FILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55342

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 23863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-0-
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 112922
LENGTH: 281
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ORGANISM: Homo sapiens
                    LENGTH: 201
TYPE: DNA
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100.0%; Pred. No.
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100.0%; Pred. No.
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2.5e-19;
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US-10-719-993-23863

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RESULT 15
US-10-425-115-124808
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                                                                                  ; OTHER INFORMATION: Clone ID: MRT4577_45300C.1 US-10-425-115-124808
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US-10-304-928-15
Query Match 0.9%; Score 25; DB 18; Length 1253; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 124808, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
                                                                                                                                                                                         SEQ ID NO 124808
LENGTH: 1253
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE OF INVENTION UNMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 1100D
CURRENT APPLICATION NUMBER: US/10/304,928
CURRENT FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yalpani, Nasser
TITLE OF INVENTION: Maize Chitinases and Their Use in
TITLE OF INVENTION: Enhancing Disease Resistance in Crop Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Simmons, Carl R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/125,915
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/522,714
PRIOR FILING DATE: 2000-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: CDS
                                                                                                                            FEATURE:
                                                                                                                                             ORGANISM: Zea mays
                                                                                                                                                                       TYPE: DNA
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  Gaps
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RESULT 17
US-10-154-419-15
; Sequence 15, Application US/10154419
; Publication No. US20030143675A1
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; LOCATION: (67)...(1491)
US-09-957-664-1
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US-09-957-664-1
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                                                                                  Query Match
Best Local S
Matches 25
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Patent No. US20020123097A1
GENERAL INFORMATION:
APPLICANT: CUITIS, ROLY A. J.
TITLE OF INVENTION: 63760, A NOVEL HUMAN TRANSPORTER AND
TITLE OF INVENTION: USES THEREFOR
FILE REFERENCE: MNI-192
                                                                                                                                                                                                                                                                                                    SEQ ID NO 15
LENGTH: 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Curtis, Roty A.J.

APPLICANT: Glucksman, Maria Alexandra

APPLICANT: Glucksman, Maria Alexandra

APPLICANT: Meyers, Rachel E.

APPLICANT: Meyers, Rachel E.

TITLE OF INVENTION: NOVEL 38594, 57312, 53659, 57250, 63760, 49938, 32146,

TITLE OF INVENTION: 57259, 67118, 67067, 62092, 8099, 46455, 54414, 53763,

TITLE OF INVENTION: 67076, 67102, 44181, 67084ALT, FBH58295FL, 57255,

TITLE OF INVENTION: AND 57255alt MOLECULES AND USES THEREFOR

FILE REFERENCE: MNI 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.9%; Score 25; Best Local Similarity 100.0%; Pred. No. Matches 25; Conservative 0; Mismatc
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CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/233,790
PRIOR FILING DATE: 2000-09-19
                                                                                                                                                                                                                                                                                                                                                                      Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 99
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/154,419
CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 4.0
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                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (67)...(1491)
                                                                                                                                                                                                                                                                                    TYPE: DNA
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ORGANISM: Homo
                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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                                                                                  Local Similarity nes 25; Conserv
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1916 AATTGACAAAAAAAAAAAAAAAA 1940
                                      2655 AATTGACAAAAAAAAAAAAAAAAAA 2679
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3337
                                                                                                                                                                                 ; ORGANISM: Arabidopsis thaliana US-09-938-842A-3337
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SEQ ID NO 3337
LENGTH: 2000
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LENGTH: 2000
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Patent No. US20020160378A1
GENERAL INFORMATION:
                                                                                          Matches
                                                                                                                                       Query Match
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Publication No. US20040009476A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR PILING DATE: 2001-08-24

PRIOR PILING DATE: 2001-08-24

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                               Local
                              2655 AATTGACAAAAAAAAAAAAAAAAA 2679
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                                                                                                                    Similarity
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                                                                                          Conservative
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100.0%; Pred. No. 0.14;
                                                                                                               100.0%;
                                                                                                               0.9%; Score 25;
100.0%; Pred. No.
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                                                                                          0; Mismatches
                                                                                                               DB 11;
0.14;
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RESULT 22
US-09-764-846-50
US-09-764-846-50
Sequence 50, Application US/09764846
Patent No. US20020102638A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and FILE REFERENCE: PTZ12
CURRENT APPLICATION NUMBER: US/09/764,846
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9622
LENGTH: 199
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-9622
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US-09-867-701-9622
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; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables US-10-719-993-6817
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US-10-719-993-6817/c
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Matches
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NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6817
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Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity 100.0%;
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APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
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NAME/KEY: misc_feature
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nes 25; Conserv
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100.0%; Pred. No. 0.
ative 0; Mismatches
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Pred. No. 0.46;
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RESULT 24
US-10-091-483-50
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; OTHER INFORMATION: n equals a,t,g, or US-09-764-846-122
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Matches
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SEQ ID NO 122
LENGTH: 222
                                                                                                                                       Sequence 50, Application US/10091483 Publication No. US20030049650A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 348
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and AntiFILE REPERENCE: PTZ12C1
CURRENT APPLICATION NUMBER: US/10/091,483
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 348
Prior Application removed - See File Wrapper or Palm SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Best Local :
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ12
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (11)
OTHER INFORMATION: n equals a,t,g, or
NAME/KBY: SITE
LOCATION: (219)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: n equals a,t,g, NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.9%;
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Pred. No.
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GENERAL INFORMATION:

APPLICANT: Schlegel. Robert

APPLICANT: Endege, Wilson

APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, ANI

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

FILE REFERENCE: MRI-007BCN

CURRENT FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 09/785,276

PRIOR APPLICATION NUMBER: 09/785,276
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US-10-091-483-122
; Sequence 122, Application US/10091483
; Publication No. US20030049650A1
                                                                                                                                                                                                                                                                            RESULT 26
US-10-357-930-20027
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, LOCATION: (219)
, OTHER INFORMATION: n equals a,t,g,
US-10-091-483-122
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SEQ ID NO 122
LENGTH: 222
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APPLICANT: ROSEN et al.
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteir
FILE REFERENCE: PTZ12C1
CURRENT APPLICATION NUMBER: US/10/091,483
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 348
                                                                                                                                                                                                                                   Sequence 20027, Application US/10357930 Publication No. US20040259086A1
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LENGTH: 222
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (11)
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LOCATION: (219)
OTHER INFORMATION: n equals a,t,g,
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ORGANISM: Homo sapiens
FEATURE:
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Local Similarity . 100.0%; Pred. No. 0.46;
es 24; Conservative 0; Mismatches
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Local Similarity 100.0%; Pred. No.
les 24; Conservative 0; Mismatch
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                                                                                                           PREVENTION, AND THE
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PRIOR APPLICATION NUMBER: 60/183,319

FILING DATE:

SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 20027

PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13

APPLICATION NUMBER: 60/219,007 FILING DATE: 2000-07-18

PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314

FILING DATE: 2000-06-09

APPLICATION NUMBER: 60/207,454

APPLICATION NUMBER: 60/189,862

2000-02-17

NUMBER OF SEQ ID NOS: 62232

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US-10-085-783A-21114 ; Sequence 21114, Application US/10085783A ; Publication No. US20040037841A1
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; ORGANISM: Human
US-10-242-535A-21114
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                                                                                                                              RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version SEQ ID NO 21114
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Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ChondroGene Inc.
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NAME/KEY: misc feature
LOCATION: 1, 2, 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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100.0%; Pr
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Pred. No. 0.46;
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; FEATURE:
, NAME/KEY: misc feature
, LOCATION: 328, 329, 330, 331, 332,
, OTHER INFORMATION: n = A,T,C or G
US-10-357-930-49814
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                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 49814
LENGTH: 413
TYPE: DNA
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Query Match 0.9%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.4 Matches 24; Conservative 0; Mismatches
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Best Local (
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PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-02-8
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PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
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TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002
                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-12-13
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                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-06-09
APPLICATION NUMBER: 60/219,007
FILING DATE: 2000-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
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100.0%; Pred. No.
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                                                                                                                                                333, 334, 335, 336, 349, 350,
                       DB 18;
0.46;
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0.46;
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                                              Length 413;
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Best Local S
Matches 24
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10672
                    SEQ ID NO 60931
LENGTH: 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 60931, Application US/10357930 Publication No. US20040259086A1 GENERAL INFORMATION:
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Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: LUDANTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/357,930 CURRENT FILING DATE: 2003-02-04
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                            PRIOR FILING DATE: 2000-12-13 NUMBER OF SEQ ID NOS: 62232
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OTHER INFORMATION: n = A,T,C or G
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                      FILING DATE: 2000-03-16
APPLICATION NUMBER: 60/207,454
FILING DATE: 2000-05-25
APPLICATION NUMBER: 60/211,314
                                                                                                                                                                   APPLICATION NUMBER: 60/219,007 FILING DATE: 2000-07-18
                                                                                                                                            APPLICATION NUMBER: 60/255,281
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Query Match
Best Local Similarity
Watches 24; Conservat
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US-10-027-632-147186/c
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US-10-425-115-129128
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US-10-425-115-129128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 129128
LENGTH: 566
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Best Local
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APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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Publication No. US20040214272A1
                                         PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT EPPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                          PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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100.0%; Pred. No.
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0.46;
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FILE REFERENCE: 38-21 (5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 124214

LENGTH: 677

TYPE: DNA
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; Sequence 124214, Application US/10425115
; Publication No. US20040214272A1
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; ORGANISM: Human
US-10-027-632-147186
                                                                                                                                                                                                                                                                                                                                                                                RESULT 35
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US-10-027-632-147186
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CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218
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Best Local Similarity
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                                                                                                                                                            APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-02-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/156,358 FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                            315 CCCTCCCAGAGCCCCGGGGGCCG 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 15; Length 635; Pred. No. 0.46; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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APPLICANT: Lewis, Marcia E.
TITLE OF INVENTION: Nucleic Acid Sequences Differentially
TITLE OF INVENTION: Expressed in Cancer Tissue
FILE REFERENCE: 1657/1032
CURRENT APPLICATION NUMBER: US/09/969,034
CURRENT FILING DATE: 2001-10-02
FRIOR APPLICATION NUMBER: 609/237,271
FRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 4494
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1012
LENGTH: 703
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SEQ ID NO 114433
LENGTH: 688
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Best Local :
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Best Local Similarity 100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                           APPLICANT: Burgess, Christopner APPLICANT: Astle, Jon H. APPLICANT: Carroll, Eddie III APPLICANT: Catino, Theodore J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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                    TYPE: DNA
ORGANISM: Homo sapiens
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Molino, Gary A.
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[00.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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RESULT 39
US-10-444-795B-796
; Sequence 796, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
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US-10-437-963-69278/c
CURRENT APPLICATION NUMBER: US/10/444,795B
CURRENT FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 842
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 796
SEQ ID NO 796
LENGTH: 844
TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 724
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Publication No. US20040123343A1
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Best Local Similarity
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                              FILE REFERENCE: 200125.449
                                                                                                                                         APPLICANT: Lewis, Stephen Patrick
TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
                                                                                                                                                                        APPLICANT: Klinghoffer, Richard APPLICANT: Lewis, Stephen Patr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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Wu, Wei
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                                                                                                                                                                                                                                                                                                                                                                            Conservative
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515,
626,
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Pred. No.
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631,
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593,
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US-10-739-930-5455/c
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; ORGANISM: Homo
US-10-723-860-5727
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US-10-723-860-5727
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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: KOVALIC, DAVID K.
APPLICANT: KOVALIC, DAVID K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
                                                                                                                                                                                                                                                SEQ ID NO 5455
LENGTH: 1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.2
SEQ ID NO 5727
LENGTH: 1486
                                                                          Matches
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Best Local Similarity
                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5455, Application US/10739930 Publication No. US20040216190A1
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APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR PILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 11088
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NUMBER OF SEQ ID NOS: 8393
                                                                                                                                                                FEATURE: OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER93891_1
                                                                                                                                                                                                            ORGANISM: Triticum aestivum
                                                                          Local Similarity
les 24; Conserv
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                                2654 AAATTGACAAAAAAAAAAAAAAA 2677
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                                                                                                                                                                                                                                  DNA
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24
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                                                                          Conservative
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Conservative (
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                                                                                        0.9%; Score 24;
100.0%; Pred. No.
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100.0%; Pred. No. 0.
ive 0; Mismatches
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100.0%; Pred. No. 0.45;
ive 0; Mismatches
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                                                                          Mismatches
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RESULT 42 US-10-425-115-119860

Sequence 119860, Application US/10425115

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RESULT 44
US-10-091-504-2292
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US-09-764-869-2292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 2292
LENGTH: 11869
TYPE: DNA
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Best Local Similarity 100.0%;
Marches 24; Conservative
                                                                                                                                                                                                                                   Sequence 2292, Application US/10091504
Publication No. US20030059908A1
GENERAL INFORMATION:
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Best Local
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LENGTH: 2192
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                    SEQ ID NO 2292
LENGTH: 11869
                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007C1
CURRENT APPLICATION NUMBER: US/10/091,504
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2442
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
-09-764-869-2292
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILLING DATE: 2003-04-28
CURRENT FILLING DATE: 2003-04-28
CURMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
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ORGANISM: Zea mays
FEATURE:
TYPE: DNA
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00.0%; Pred. No. 0.45; 
ve 0; Mismatches 0; Indels
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Query Match
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US-10-227-577-2292
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Best Local Similarity
Matches 24; Conserv
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2292
LENGTH: 11869
                                                                                                                                                                             Sequence 1095, Application US/10292798 Publication No. US20030235833A1
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Publication No. US20040005575A1
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CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/091,504
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 09/764,869
PRIOR FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PC007C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/764,869
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
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PRIOR FILING DATE: 2000-08-14
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APPLICATION NUMBER: 60/217,496
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100.0%; Pr
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100.0%; Pred. No.
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1095
LENGTH: 358246
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PRIOR FILING DATE: 2001-12-18
                       NAME/KEY: modified base LOCATION: (2818)..(2917) COTHER INFORMATION: a, t,
                                                                                 NAME/KEY: modified base LOCATION: (1659)..(1758) OTHER INFORMATION: a, t,
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\mathtt{NAME}/\mathtt{KEY}: \mathtt{modified\_base}
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ORGANISM: Homo sapiens
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OCATION: (291513)..(291770)
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OCATION: (29165)..(29206)
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OCATION: (201)..(326)
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CCATION: (133049)..(133353)
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OCATION: (72539)..(72763)
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(343822)..(344071)
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(330441)..(330609)
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(261460)..(261526)
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(325058)..(325316)
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(302538)..(302800)
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(337750)..(337828)
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(291173)..(291325)
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FEATURE:
NAME/KEY: modified base
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LOCATION: (131002)...(131002)
OTHER INFORMATION: a, t, c,
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LOCATION: (130997)...(130999)
OTHER INFORMATION: a, t, c,
FEATURE:
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OTHER INFORMATION: a, t,
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LOCATION: (130984)..(130984)
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NOCATION: (130979)...(130979)
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LOCATION: (130976)..(130977)
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LOCATION: (130963)...(130964)
OTHER INFORMATION: a, t, c,
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LOCATION: (81210)...(81309)
OTHER INFORMATION: a, t, c
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LOCATION: (77979)...(78078)
OTHER INFORMATION: a, t, c
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LOCATION: (51382)..(51481)
OTHER INFORMATION: a, t, c
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OTHER INFORMATION: a, t, c,
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LOCATION: (17497)..(17497)
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LOCATION: (71021)..(71120)
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LOCATION: (17518)..(17518)
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COCATION: (131025)..(131025)..(131025)..(131025)..(131025)...(1310 NAME/KEY: modified_base

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Best Local
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                                                                                                                                                         APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
                                             PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
             PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
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LOCATION: (131127). (131129)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (131063)...(131063)
OTHER INFORMATION: a, t, c,
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LOCATION: (131065)...(131065)
OTHER INFORMATION: a, t, c,
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LOCATION: (131048)..(131049)
OTHER_INFORMATION: a, t, c,
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LOCATION: (131034)...(131034)
OTHER INFORMATION: a, t, c,
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LOCATION: (131031)...(131031)
OTHER INFORMATION: a, t, c,
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LOCATION: (131090)...(131091)
OTHER INFORMATION: a, t, c,
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OTHER INFORMATION: a, t, c,
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LOCATION: (131059)..(131060)
OTHER INFORMATION: a, t, c,
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100.0%; Pred. No. 0.41;
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US-10-741-601-22073
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US-10-741-601-22073/c
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SEQ ID NO 54104
LENGTH: 160
TYPE: DNA
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                                                                                                                   NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 22073
LENGTH: 201
TYPE: DNA
                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1500
CURRENT APPLICATION UNMEER: US/10/741,601
CURRENT FILING DATE: 2003_12-22
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SEQ ID NO 54104
LENGTH: 160
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Best Local Similarity
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TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
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PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
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  Local Similarity 100.0%; I hes 23; Conservative 0;
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0.9%; Score 23; DB 17; Length 201; 100.0%; Pred. No. 1.5; Indels
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100.0%; Pred. No.
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RESULT 50

US-09-867-701-9978

Sequence 9978, Application US/09867701

Patent No. US20020132237A1

GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Haglate, Paul A.
APPLICANT: Haglate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9978
LENGTH: 222
TYPE: DNA
ORGANISM: Homo sapien
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Search completed: January 15, 2005, 12:52:34 Job time: 1458 secs
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                                                                                                                                                          Query Match 0.9%; Score 23; DB 9; Best Local Similarity 100.0%; Pred. No. 1.5; Matches 23; Conservative 0; Mismatches
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